

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCACATGTTGGCTGCAAGGCTGGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCAGCCTTTCACCAAGGCCCTCCCTGTTGTGGAAGAAATTCATCAGCAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCACCAACAGAAATTTGGGATCCGGCGTGGGA
 GAACTGGCCAAAGAACTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAAAT
 GATCAGATGGGAAGATGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTTCATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTCGTCTTTGTGTCCCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCCTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCCTTTTTCAGCATGTTCCCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTTAAATATATTTATGCGAGTTGCAACTATGCTGGCACTGGAGGCAACAGAAAGAAATTG
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAAATATCTGTTTAAATGGGGCAGATATGC
 ATTTAAATAGTTTGTACAGAGCAGCTTTCGTTGAAGTTTGAAGAAATAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTTTCTGGAGAATAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTCCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAGTTTGTGTCATGAGAATGTAAGTCTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACTAAAATTTAGCAAACTGTGTTTGCATATTTTTTGGAGT
 GCAGAAATTTGTAATTAATGTCATAAGTGATTGGAGCTTTGGTAAAGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTGGAACCAAGTGGTCATTGTTACATTCAATTT
 GCTGAACTTAAACAAACTGTTTCCTGAAACAGGCACAGGTGATGCATTTCTCCTGCTGTTG
 CTCTCAGTGTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAAATGTTAATC
 ATACAGAGAACTCTTGATGAATTATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
 AATAACAAACAGTATATCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWFQYVKDRI
HSTYMYLAGSIGLTALSAIAIS RTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGTCTCCGCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCCGCTCGTGAGGG
 GGTGCGGACAGCGGGAATCGGGCGGCTTGTGCATCTTGCTACCTTGGGTCGAAGATGTCGG
 ACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCAGCGGCTATTGGTTCCGCGCCACCGCTC
 CGCGTGCCCTTGGTCGGCAACATCGGCGCTCATCAGCCCGGCTACCTCTTCCCTTGGCCCGA
 AGCCTTCCCTTATCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTATTTCCCTGTGG
 GTCCAGGAACATGGATTCTTTATTTGGTCAATTTATTTCTTATATCATGATTTCTACGCGA
 CTTGAAACAGGAGACTTTTATCGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTGTGATCGTGATTACTGGCTTAGCAATGGATATGCAGTTCGTGATGATTCCTCTGATCA
 TGTCAGTACTTTATCTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTGGA
 ACACGATTTAAGGCCCTGCTATTTACCTGGGTTATCCTTGGATTCACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCCCTAATGTTCA
 GATACCCCAATGGACTTTGGGAGGAAGAATTTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGAGAGTATCAGGATTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
 TGTGATCAGAAATGCGGAGCGGAGACACAACCTGGGGCCAGGCTTTCGACTTGGAGACC
 AGTGAAGGGCGCGCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCTCCAGTGTGGGTG
 CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACTGAATGTAGTCTTTC
 AGTAGAGACAAGATTTCTTAAATCCCGCAAGAAAATATAAGTGTCCACAAGTTTCCAGAT
 TCTCATTTCAAGTCTTACTCTGTGAAGAACAATAACCACTGTGCAAAATGCAAACTGAC
 TACATTTTTTGGTGCTCTCTCTCTCCCTTTCCGTCTGAATAATGGGTTTAGGGGGTCTCT
 AATCTGCTGGCATTTGAGCTGGGGCTGGGTACCAACCCCTTCCAAAGAGCACTTATCTCTT
 TCTTGCACATGCTCTCTCTCCACTTTTCCCAACCCCACTTTGCAACTAGAAAAAGTTG
 CCCATAAAATGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAAGGCTGGT
 ACAACAACATATTCAGGTTATTTTCCCTTTTGGTGGCAGAAGTTTACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCCTTTCTCAGCTTTTGGAAATGCTTCGACTGCATCCGTTGTT
 AACCGTTTCCCACTCTTCAGATATTTTTATAAAAAAATACCACCTGAGTTGATGAGGGCA
 CAGATTGGTTATTATGAGATACGAGGTTGGTCTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAAGACTTAGTGAGCTTGACGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
 TTGGCTTCTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
 ATTCCATTTAAATCTCACTTTTTTGCCTATCCCCGTTTTTGGTCATGTTTCAATTAATTGT
 CGCTATTTAAATCTCACTTTTTTGCCTATCCCCGTTTTTGGTCATGTTTCAATTAATTGT
 GAGGAAGGCGCAGCTCTCTCTGCACGTAGATCAATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATACATGATTTAAGGTTGAAATGGCTTTAGAATCAATTTGGGTTTGGAGGTGTGTTA
 TTTTGAGTCAATGAATGCAAGCTCTGTGAATCAGACAGCTTAAATACCCACACCTTTTTT
 TCGTAGGTGGGCTTTTCCATCAGAGCTTGGCTCATAACCAAAATAAGCTTTTTTGAAGGCCA
 TGGCTTTTACACAGATTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCGAT
 ATTGAGTGCTGTCACTTTTGGAGCAACTAAAAGGCTTCAAACGTTTGTATCAGTTTCTT
 TTCAGGAACATTTGTGCTCTAACAGTATGACTATCTTTCCCCACTCTTAAACAGCTGTGAT
 GTGTGTTATCTAGAAATGAGAGTTGGCAACAACCTTCTCATTTTGAATAGAGTTTGTGTCA
 TACTTCTCATATTTAATTTATATGATAAAATAGGTGGGAGAGCTCGAAGCTTAAGTGTCA
 TGTTTTGTGTCTCATCTGTGGCCACAATAAAGTTTACTTGTAAATTTTAGAGGCCATTACT
 CCAATTTATGTTGACGTATCACTCATTTGTACAGGCGTGGAGACTATGTATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCTCTTACCAGTCAGCTGCCTGCGAG
 CAGTCAATTTTCTTAAAGTTTACAAGTATTAGAAGCTTTAGAAGTTCAGGCAAAAATGTTT
 ATGAAGTATTCTCTTAAACATGTTTAGGAAGCTGATGAGCTTATGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACAAAACAGCTATTTGAGTTTGACTTGACAGGCAAAAACA
 TGACAGTGGATTCTCTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTAAACTAATCCTTTTTATTTGGTAAAAATGTAAATTAATATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRADQNGGGGRHNWGQGFRF
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

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FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCCAAAGGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCGTTGCC
 CCTTTGGGGCGGG**ATG**GCCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTCGCAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAAGGTCTGAACTTCCTCCCTCC
 CACAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVVEIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEESKLTYTEIHQYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAIEDFTIFKAMMVQKNIEMLQAIIRIIQERNGLVLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

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FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGAGGTAATTAAGAAAC
 AGTGGAAATGGGAAAAACAGTGGCTGTAGTCATCTGTAAATATGCTCCTGTGCAACAAATGTATAC
 ATTCTGCTAGGTGCCATATTCTATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAACAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCTCGCT
 TTTCTTTATTTCTGGATAAATCTGATTGCTTCTATGTCTGTCTTCTTCAACAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCTCAGGATAGTGTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTTGTCTATTGTGGCCCT
 TGACTGCCGGGATAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTCAGCCCTTCCAAATTCCTGCTCTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCCTAGGAAGCATCTTCATACA
 GAACAGCAAATCTATTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGTAGTATGAAGACTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTGTAACTGCATTTCCAGGGCCCTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGTATGGCCAGGTTACCACTGTCTATTATCAACAAGAGTGTCTGTCCCTG
 TCTTTGACTTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCATCAGTCTCTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCTCAAGTTCGGGAATACGCACCTAGGCAAGAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTTATTTTTCACATTTTCAGTGTGTGTAATATTATCTTTTCACTTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGTCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAGGCTAAGAAATTTCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTTGGCCTTCAAGCTTCCAAAAAACTTGTAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 CTCTCCCTTTTAAACATTATAAAAGCTAGGTTGCTCTGTAATTTTGAGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAAATTTTTGCTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAAATTTTAGAAATTCATGGGAAATTGGATTTTTGT
 AATAATCTTTTGATGTTTAAACATTGGTTCCTCTAGTCACCATAGTTTACCCTTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAAGAGAAAAATCTTGAT
 GTCATTACTCCTGAATATTACATTTTGGAGAATAAGAGGGCATTTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATCTTTCCAAGAGTTGAAATGTGCTGCTTCAGATCATAC
 CAGATTGTGCAGTGAAGCTGATGCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAACACATGTTGACTTTTAACTGATGTATGAATATTAACTCTAAAAATAGAAAGACC
 AGTAATATATAAGTCACTTTACAGTGCTACTTTCACACTTAAAGGTGCATGGTATTCTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAAAACAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATACTGTAATATGAGCTTTATGGTGT
 CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTCATTGTGATATCCACAATAATATGACTGGCAAGAATTG
 GTGGAAATTTGTAATTAATAATATTATAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPMAMV
IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSASFVALI
FVTAFQGLSVAFILKFLDNMFHVILMAQVTTVTIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAACTTTA

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FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCAGAGGAGCAT
 CCGGTCTACAGGTCCCAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCATGAACGCGCGGCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCTCTCAGATCTAC
 CTATTG**CATG**TGGCTCAGGTGGGCCCTTCTCTGCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCAGAGACCCCTGGTGGGCTCTGCATCAGAAATCCCCTGGACCTGCC
 TGGGTCGCCCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTCATTGCCTACTTCTCT
 ATCTGGTTTCGTGCCCCGACTTCCACACGGCCAGACCTATGGTACCTGCTTTTCTATTGCCCT
 CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCCTTGTTCACAG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATAACATGGCACCACTTTCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTCCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAATT
 ATTACTGGCTTCTCTTACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCCATCTGGCAGTGGTCTTGTACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTAC
 TACCCTGGTCCATGCTGCCGTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGCTTCTTCAACAAGTTTGCTCTGGAGTGTG
 ACTGGGCATTTCTACCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTTCTCATCCTG
 CTGGGCTGCTGCTTCAAATGTACCCATTGATGAGGAGAGGCGGCGGCAGAAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTC**TAG**GGGCCCGCCACGTTGCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCCTGTGCTCACTGTGGGGCCGGCTGCTCTG
 TGGCCTCTGCTTCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGCTGATGGGCTAGCCCGGAACATAATGTAGAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

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FIGURE 12

MWLRWALS LPPSSCLWAE PGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIP IWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLG LLLFKMYPIDEERRRQNKAL
QALRDEASSSGCSETDSTELASIL

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FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

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GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTC
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTTATA
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTATGTTCTGTTATAAGCAAGTTCATGCTCTGAGTCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
ACTTTCATATTGTGGCAAACCTTCAGAAAAACAACCCTTTTTGCCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
CAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGTCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAAAACCTCCATTGGAACCCCCAGGACAAAGGTTATGTGCTTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCTTCTTTGGTTTTTCTTGACTTACATTCTGTA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTCAGTAAAGGAT
AAAATATTTCTGTAATGATTATGATTTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
TTCCTCTGCGAAATTTCAACCACCTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAACACTGAAGAAGCCATTATAGATAGTATTCTAAAGGATGATCATCAAGAAGACTA
TTAAAACACCTATGCTCTATACCTTTTTTATCTCAGAAAATAAAGCTCAAAGACATAG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

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FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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CCACGCGCTCCGCCGCCGCTGCTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGCGCTGCAC
CTTCGCCTTGTACTTGCTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
AGGCTGGAGGAGGTGCTGTGGTTCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCTGCTCTTCGCGGCCTA
CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGACCTCGGTGGGTGCCACATGC
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
TGAGACTTTTCCCATGACACAAACTGGTTCCTGAACCTCTCGGCCCAATTCTGAACATT
CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCACTGTGT
GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGATGTCTTTTCTCCTGGGACACTG
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAAAAAATT
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAAGA
CACATGCACTCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
TGTGGTCCCTAAAGCCCCCTCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCTAGAAAAATGCTGTTTGT
GGCCGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
ACAAGGTCAGGAGTCTCAAGACAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
ACAAAAATTAGCCAGGCGGTGGTCAGGCAGCTTGCAATCCAGCTACTCGGGAGGCTGAGGC
AGGAGAAATTGCTTGAACCAAGGTGGCAGAGGTTGCAATGAGCCAAGATCACACCAGTGCAT
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
KEHQAYVFLFCGAYLYKQGFAIPGSSFLNVLAGALFGFWLGLLLCCVLTSVGATCCYLLSS
IFGKQLVVSYPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

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FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGAC**ATG**GATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGAAAAAGAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCATTCTGCC
 AACTGCACTGGCTGTGCCAGAAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCTACTCACTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGT**GAG**GAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAA

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FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPYPLLIIVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLEDA PRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAAATACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGATTTTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

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FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACCTGGTGGCCAGCTGCTAGACCGTGCCCTATGAGCCGCTGGGGCTGCAGTGGGGACATGCC
 CTCCTCGCCACCCCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 ACCCGAATGGCGCCACTTCATCGACAACAGGTTACAGCCAACTGTCAGGATTCGAATG
 GACACGTATGCTTAAGAGCCACGACCTTATGTGAGTTTCTGGAACTGCTATGACATGCT
 TATGAGCAGTGGGCGAGCGGCCAGTGGGAGCGGCCAGAGTCTGCGGGCTCCAGGAGC
 TGGTGCTGGAACCTGCGCAGAGCGGGCGGCCCTGGAGGGGTACGCTACAGCGCAGTGGT
 AAGCAGCAGGCAACGCGACACTCCATGGCCCTGCTGCAGTGGGGGGCTGTGGCGCCAGCT
 CGCCAGGCCATGTGGGGCTGGGCGCTGAGGGGACACTCCATCCCCCGCTGGAAACTGTCCA
 GCGCCGAGACATATTACGCATGCGCTGGAAGCTGCTGCCAACCTACCTTCAGCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACCAACCCAGGAGGCG
 CTCACCTGCTTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCCACCGAGTTGCTGCGAGG
 AGGACACGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGACTG
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGGCCGAGTGCCAGCTGGTGACCGGTAGTGGCGGT
 GGTCCCAGGGCTGCTGGAGGCTCACCACACAGAATCTATACTTCTACGATGCGAGCACTGAGC
 GCGTGGAACCCGAGGAGGCGATCGGCTATGATTTCCGGGCCCACTGGCCAGCTCGGTGAG
 GTCCACCTGGCGCGTTTCAACCTGCGCGGTTTCAGCACTTGAGCTCTTCTTTATCATCAGGC
 CAACTACTTCTCAACTTCCCATGCAAGGTGGGCACGACCAGCTCTCATCTCCTAGCCAGA
 CTCGAGAGCCCCAGCTGGCCCCATCCCAACCCATACCCAGGTACCGGACAGGCTGATCTCG
 TGGCTCTGCGGCTACGCGCCCCCTCTCAAGGCTACCTAAGCAGCTCCGCCAGGAGAT
 GCTGCGTGCTCAGGGCTTACCCAGAAATGGGTACAGGCTGAGATATCCAATCTCGAGATAT
 TGAATGCAACTCAACCAATTGGGGGGCGGACCTACAATGACCTGTCTCAGTACCTTGTTCT
 CCGTGGGTCTTCAGGACTACGTGTGCCAACCTGGAGCTCAGCAACCCAGCGCTCTTCGG
 GGACCTGTCTAAGCCCTATGGGTGGTGGTGAACCCAGCAATGCCAGCTCGTGAGGAGAAGT
 ATGAAGCTTTGAGGACCCAGCAGGAGACCATTGACAAGTTTCCACTATGGCACCCACTACTCC
 ATGACAGCAGGCGGCTGACCTACCTCATCCGCTGGAGGCTCTCACTCCCTGCAGCTCCA
 GCTGCAAGTGGCGGCTTTGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGCACTCTGGC
 AGGCAGCGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCGGAATTTCTTACTTTCTCT
 GACTTCTCGGAGAACCAGAACGCTTTTGACTGGGCTGTCTCCAGCTGACCAACGAGAGAGGT
 AGGCGATGTGGTGCTTACCCCGTGGGCGAGCTCTCTGAGGACTCATCCAGCAGCACCGGC
 AGGCTCTGGAGTCGGAGTATGTGCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGAGCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCGAGACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAATCGGCTCTCA
 GCTGAGGAGAGCGCCCATCGCTTGCAGCGCTGGACACTAATCACTAGCATCTTCCAGCA
 CCTGGACGAACCTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGCCAGTGGGCTGTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTCACTTCAGCTCAGCAAGAGCCCT
 ACCATGGGCGGCCACAAGACGACGACGACTGCTGAGTGGCCCCGTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGAGTGGAAAGCTGCTTATTCAGCGGTGGCCACTGGG
 ATGCTGCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCACCTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACTGCATGGTGTGGCGGCTCTGCATCAGGGTGGTCTGTCTCAGTAGGCCCTGGCAG
 CAAAGCCTGTGCAGGCTCGTATGGGCATGGGGCTGCAGTGAAGCTGTGTGGCCATCAGCACT
 GAACCTTGACATGCTGTGTCTGGATCTGAGGATGGAATGCTGATACACATGTACGCGG
 CGGACAGTTTGTAGCGGCGACTACGGCCTCTGGGTGCCACATTTCCCTGGACCTATTTCCACC
 TGGCATTGGGGTCCGAAGCCAGATTGTGGTACAGAGCTCAGCTGAGGAGCTCTTGGGGCC
 CAGGTCACTACTCTTGCACCTGTATTGATCAATGGGAAGTTGGCGGGCTTCACTGCCCT
 GGCAGAGCACTCTCAGCGCTGACGGTGACAGAGGACTTTGTGTTGCTGGGACCGCGGCTGA
 GCGCCCTGCACTCTTCAACTAAACACACTGCTCCCGGCCCGCGCTCTCCTTGGCCATGAAG
 GTGGCCATCCGACAGCTGGCCGTGACCAAGGAGCGCAGCGTGTGGTGGGCTGGAGGA
 TGGCAAGCTCATCTGCTGGTGGTCGCGGGGCGAGCCCTCTGAGGTGGCGAGACGAGTTCGCG
 GGAAGCTGTGGCGGTCCTCGCGGCGCATCTCCAGGTTCTCTCGGAGAGACGGAATAACA
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCGCGCCCGGCGAGGCGCT
 GCGCGGAGGACCCCGCCAGAAGTCCGCGGGAACACCCCGGCGGACCGGAGGCGGTGA
 GCGGGGCCCAACCTGCGCCAGCTCAGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCCGCCTCGCCGGCTGAGGGGCGCGCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQAQHSMAALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSSPSTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPSPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKEIP
 EFFYFPDFLENQNGFDLGLQLTNEKVGDVVLPWPASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSEAAEAHRLARLDNTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGMSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLLISGSRDTCMVWRLLHQGGLSVGLAPKPQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGIQVQSSA
 WERPGAQVTVSYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

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FIGURE 24

CCGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCACCTTGTGAACCTCTCGTGCCCAGGGCTGATGTGCGCTCTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAACTCATGSGGCTCTGGGGCTCTTC
 TGGACCCTTAACCTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCTGCTTGGACAAAGTCACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTTCGAGGCGTGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTATCGCCAGCGGCTTCTTCAGCGT
 TTTCCGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCAACGCTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAACCTCC
 GTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCACTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTCAGTGAAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAA
 AAGATTTTATTAAGATATTTTGTAACTC

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FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLE
WTLNWWLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCGCGGGCTCTTGTTACCTCAGCGCAGCGCCAGGCGTCCGCGCCGCCGT
 GGCT**ATG**TTCGTGTCGATTTCCGCAAGAGTTCTACGAGTGTTCCAGAGCCAGAGGTCC
 TTCTCTTCGTGGCCTCGGAGTGGATGCTCTGTGTGCGTGAAGATCCTTCAGGCCCTTGTTT
 CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACAGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGTTGATGTTTGTGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACAACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTTCATTTTGGGTTCAAGCACAAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAAGCTCGCAAGAAGCAGCTGCGAGCCACCCAGCAGACATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTCTGACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCTGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAACACCTGCTCA
 AGTCCTTTGTGTGTTTCGACAAAGAACCAGGCGCTGCAAATGCTGCCCTTGGTGTGGTGGC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCAGCAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGAAGCAGCGGAAGCACCAGCTCCCGGA
 TGCTGCAACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTTAGATTGAAGTTATGGACATGATTGTAGATGTAGAAGCCATT
 TTTTATTAATAAATGCTTATTTTAGGAAA

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FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDI FRDEEEDEEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEFADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFCVSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNFDLSVIELKAEDRSKFL
DALISLLS

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FIGURE 28

GTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCGGATTTCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

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FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTCTAGTGAAC
 CACGAAGGGACGTATACCAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTCTTTGGAAAGCTAA
 GTCTCTCCCTTTATCGAGTCAAGAAACCCCCCTCTTTGAGCTATTTACAGCTTTTAAACAATT
 GAGTAAAGTAGCTCCGGTCAAC**ATGG**TGACAGCCGCCCTGGGTCCCGTCTGGGACGGCTC
 CTGCTCTTTCTCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCATGTATCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCCGTGAGATCAGACCCCTACATTAATATCAGCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCTGCCAGGGTACATGGGCAGGGAGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGCGAGCAAGGGTGACAAGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GGCAGGACTTCCAGACGCTGTCTTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACGGCCAGTTTGTCTGCTCCCTCGGTGGCATCTACTTCTTCAGCCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCCAGAAAGAGGCTGTCTATC
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGACAGAGCCAGAGTGTGATGCTGACCTGGC
 CTACGGGGACCCGCTCTGGGTGCCGCTCTTCAAGCGCCAGCGGAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACT**GA**GGG
 CCTCTGGGCCACCTTCCCGGCTGGAGAGCTCAGGTGCTGTCCGTCGCCCTCAGGGGCTCAG
 TTTGACCTGCTGTGAAGAGCTTGAAGCCAGGAAGGCCAGGGAGTCCCCGGGAGCTGGCTTCTGGGAGA
 CCGTCTCTATCTTTGGCTGCCATCATCCCTCCAGCCCTATTTCTGTCTCTCTCTCTCTCT
 TGGACCTATTTAAGAAGCTTGTAACTTAATATTTCTAGAAGCTTTCCAGCCCTCGTAGCCCC
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGGTTCGTGTAAATGCAGATTCT
 GACTCAGCAGGCTCTGATGGGTCCAGGATTCTGTGTTTCTCATATGTTCTCTGGGTGATGCTG
 ATGGGGTCACTATGAACCACTGGAGCAACAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATCTTGAATCCTCCCACTTCTAGAATTTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTGTCTGTGTCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCTACTGTG
 AACCTCTGCCCTCCGGGTCAAGGATTCTTCTGCCCTCAGCCCTGCCATGTGGGTGGGATTAC
 AGGGCCCTGCTACCATGCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCCACATA
 TTTGGCCAGGCTGGTCTTGAACCTCTGACTTCAAGGTGACCCACCCGCTCGGCCCTCAAAAT
 GCTGGGATTACAGGTGTAGCCACCGTGCCTGGCCAAATCCAACATTTCTAAATTTCTCTCAT
 CCTCTCCAGGCTCCCGGTGCTATGTTCTCTTTACCCCTTCCCTCTCTCTGTCTCAGGCC
 TGCACCACTGCAGCCACCGTTTCAATTTATTCATTATTAACACTGAGCACCTACCTCTGTGCT
 GGGTCCCGGGAAGGGTGAAGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTGACTGGCCCA
 GTCCAGCCAGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTCTCAGGTGCTGCTGGTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGCAAGTATCTCTCTCCCGTTCCTCATCCACCTGCCGAC
 TGCTCATGTGTACAGCAAAACCCAGGGGGCTTGGCCAGGTCAAGGGTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCCAGAAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTTGCAGAAAGACCTCTCCCTCACTGGGATCCC
 CTTCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGTCTCAGTCCCTTCCACCAAGTCACTCT
 GAACCTCCGTTTCCCGAGGCCCTCAGCTGCCCTCAGACACTGATGCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCCCTCTACCCGGCCAGTGCCCGACTCTCAGGCTTTATCAAGGTTG
 CTAAGGCCCGGTGGGCAGTCTCTCGTCTCAGAGCCCTCTCCGGCTGGTGTGCCCTTTAC
 AAACACTGTCAGGAGAAGGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAAGGAGGGACCTCAGGCCCTCCGTTCTTCTTCCAGGGTGGGGTGGCCTGGT
 GTTCCCCTAGCCTTCCAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGGCGCCCTCCG
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTCCCCGGGGGTGATCTTGTGTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTGTGACCAAGTGCACGGA
 AGACTGTGCTATAAACCCCTCGCTGATCTGCTGCCCTGACCCGCCACGCCCCCTGCC
 GTCCAGCATGATTAAGAATGCTGTCTCCTCTTGAAAAA

FIGURE 30

MVTAALGPVWAALLLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPETRPYINITILKGDKGDPGPMGLPGYMGREGPQGEFPGPQSGKDKGEMSGPAPCQKR
FAFSVGRKTAHLSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSQVMOLDLAYGDRVWVRLFKQRKENAIYSNDFDTYIT
FSGLHIMKEADD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCAGCCGCCAGGAAAGACTG
 AGGCCCGGGCTGCCCGCCCGGCTCCTGCGCCGCGCGCGCTCCCGGGACAGAAAG**ATGTG**
 CTCACAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCAGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCGGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCGGGCTGCCGGGCTGCAGCTCCTGGACCTGTTCAC
 AGAACCATGCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATCACCAATGAGACCTTCCTGTGGCTGCGGCGCCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACACAGAGCTCGGGCACTGCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGAG
 AGGGGCTCTTACGCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTTGACGCGCTGCGGCTGGCCGGCAACAC
 CCGCATTTGCCAGCTCGGGCCCGAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTTAAGCTTGCAGGCCCTGCTGCGGACCTCTCGGGCTCTTCCCGGCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTG
 GGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACACC
 ACCACAGCCACAGTGCCACCACGAGGCCCTGGTGGCGGAGCCACAGCCTTGTCTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCTTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCAGCTTGCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACACCTGGCGTGTGTGGCCCCAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGTTGAGCCCCACCTCCCTGCGC
 GTGGGGCTGCAGCGTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTACATGCTTTGGG
 CCCGGGCGGGTGCCGGAGGGCGAGGAGGCTGCGGGGAGGCCATACACCCCCAGCCGTCCA
 CTCCAACACGCCCCAGTACCCAGGCCCGCGAGGGGCAACCTGCCGTCTCTATTGCGCGCG
 CCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACAGCTACTGTGTGCGGCGG
 GGGCGGGCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCGCT
 GGAATCGAGGGAGTGAAGGTCCCTTTGAGGCCAGGCCGAAGGCCAACAGAGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCTGGCCTC
 CAGTCACCCCCTCACGCAAGCCCTACATCT**TAAG**CCAGAGAGAGAGAGGCGAGCTGGGGCGG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACAGCTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCTATGAGGACAGTGTCCGCGCTGCCCTCCGCAACGTGCAGTCCCTGGGACGGG
 GGCCCTGCCATGTGCTGGTAACGCATGCCGGGTCTGCTGGGCTCTCCGACTCCAGCGGGA
 CCTTGGGGGCGAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGATAGCGCGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGAGACAAGCTTTGGTTTTTGAAGACAAACGATGATAG
 AAGGCCCTTTTGAAGAAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVP LLLPL LLLLLLALGPGVQGCPSGCQCSQPQT V FCTARQGT TVPRDVP P DTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLP SGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNE LRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLG LQQ LDEGLFSRLRNLDLHDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFG
PWVRESHVTLASPEETRCHFP PKNAGRLLLELDYADFGCPATTTTATVP TTRPVVREPTALS
SSLAPT WLSPTAPATEAPSP P STAPPTVG PVPQPD C P P STCLNGGTCHLGTRHHLACLCP E
GFTGLYC ESQMGGQTRPSP TPVT PRPPRS LTLGIEPVSP TSLRVGLQRYLQGS SVQLRSLRL
TYRNLSGPDKRLVTLRLPASLA EYTVTQLRPNATYSVCV M PLGFRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNPLLIAPALAAVLLAALA AVGAAYCVRRGRAMAAAAQDKGQVGP GAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP GGLQSP L HAKPYI

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FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATTCATTCATGAGGAAATAGTGGTAAATCCTTGGAAATAC**AATG**AGACTCATCAG
 AACAACTTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGGTGTCCCGAGACTTG
 AAGAAAGGGAACCTGATGACCAACTGCTCCAACATGCTCTAAGAAAGGTTCCCGAGACTTG
 ACCCCAGGCCACACGACACTGGATTTATCCTATAAGCTCCTTTTCTACTCCAGACTTCAG
 TTTTCATTCTGCTCCAACTGAGAGTTTGGATTCTATGCCATAACGAATTCACAGCTGG
 ATCTCAAAACCTTTGAGTTTCAACAAAGGAGTTAAGATTAGATTGCTTATAACAGACTG
 AAGAGCTPAACTTGGTATTTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAACTGAT
 TGACACCATGCCATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCAGAAAAATGCTCATCTGCAATCTAAATACCTTC
 TTCCTAGGATTCCAGAACTCTCCCTCATTATGAAGAAGGTAGCCTGCCATCTTAAACACAC
 AAACTGCACATTTGTTTTACCAATGGACACAATTTCTGGGTCTCTTTGGCTGATGGAATCA
 AGACTTCAAAAATATTAGAATAGCAAAATATAGATGGCAAAAGCCAATTTGAAGTTATGGA
 ATGCAACGAAATCTTAGTTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAAATAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACTCT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAACTTCAATTGACTAC
 TCAAAATCTGTAATGAGAATAATAAAATTTGGAGCATGTACATTTTCAAGTGTTTTACATCA
 ACAGAGTAAAACTTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATATCAATG
 CACAAATGGCCACACTGCTTTTCCGAATTTCTACGAAATTTCAATATTTAAATTTTGGC
 AATAATATCTTAAACAGCAGGTTGTTTAAAGAACTATCCAATTCGGCTCATTTGAAACTCT
 CATTTTGAATGGCAATAAATCGGAGACACTTCTTTAGTAAGTTGCTTTGCTAACACACAC
 CCTTGGAAACACTTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAATTTGCTCA
 TGGCCAGAAACTTGGGTCAATGAATCTGTCATCAATAAATTTGCTGATCTGCTCTGCTG
 GTGCTTGGCCAAAGATTTCAAATACTTGACCTAAATAATAACCAATCCAAACGTGACCTA
 AAGAGACTTATTCATCTGATGGCCTTACGAGAACATAAATTTGCAATTTTCTTAACTGAT
 CTCCTGGATGCACTTTCAGTAGACTTTTCAAGTCTGAACTTGAATGAACTTTCATTCT
 CAGCCCATCTCGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATCGCGGAAGAA
 ATCCATTCGGGTGTACCTGTGAATTAATAAATTTCAATTCAGCTTGAACATATTCAGAGTCT
 ATGATGGTTGGATGGTTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACCTAG
 GTTAAAGACGTTTCATCTCCACGAATTTATCTTGAACACAGCTCTGTTGATTGTCAACCTAT
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAACACACCCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCAATTTATTTCAACAGTGAACATGATCTC
 TGTGGGTGAAGATGAATGATCCCCAATCTAGAGAAGGAAGTGGTTCTATCTTGATTGCT
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGATGAGTGGTGCCATT
 ATGAATTTCTACTTTGCCACCACAATCTCTTTCCATGAAAATCTGATCATATAATTTCTTATC
 TTACTGGAAACCCATTCCATCTATTGCTATCCCAACAGGTATCATAACTGAAAGCTCTCTCT
 TGAGAAAAAGCATACTTGAATGGCCAAAGATAGGCCGTAAGTGGGGCTTTTCTGGGCAA
 ACCTTGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACGTGCAGACA
 TTCCAGAGCTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGTATGAGAACAGATTGGCTCT
ATAAAATCCCAAGCTCCTTGGGAAGTTGGGGACCATACACTGTTGGGATGTACATTTGATA
CAACCTTTATGATGGCAATTTGACAATATTTTAAATAAAAAATGGTTATTCCTTCATA
TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTTCACAGTTTATAAGG
GCTTATGGAAGAGGTGTTTCAATCCAGGATTTGTTTATAATCATATAATGTAATATAATATA
AGTGGCTCACTCTGTAATCCCAGCACATATGGGAGGCCAAGGTGGGTGAGCCACAGGTCAA
GAGATGGAGACCATCTGGCCAAACATGGTGAACCTGTCTCTACTAAAAATACAAAATTA
GCTGGGCGTGTAGGTGCACGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGACAGGAGATCG
CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGGCCTGCATCTCCAGCTGGT
GACAGGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAAGAAATATCC
TCAATGGCCACAAAATAAGGCTCAATTCATAAATATAGTACATTAATGTAATATAATATA
CATGCCACTAAAAAGATAAGGTAGCTGTATATTTCCCTGGTATGGAAAAAATATTAATAT
GTTTAAACTATTAGGTGGTGCAAACTAATTTGGGTTTTGCCATTTGAATGGCATGTGAA
ATAAAGGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTTGGGAGGTTGGA
TTACAGGAGCATTTGATTCTATGTTGTGATTCTTATAATGTTTGAATGTTTAGAATGA
ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQLDLKTFFENKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILTDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLQHKNDENCswPETVvNMNLSYNKLS
DSVFRCLPKSIQILDlnnnQIQTVPKETIHLMALRELNIAFNFLTDLPgcSHfSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTtQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHNNLFHENSdHIIlILEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

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GGGGGGCTTTCTTGGGCTTGGCTGCTTGAAACACCTGCTCCAGAGACCGGCCTCGAGAGGGTTCGCGGGGAAAGG
GAGGGAGAGAGGAGGCGGGGGCGGGCCCCCTCGCGCCGCCCGCGGCTCTCGCGCGCCCTTGCCTGGCGCGCGC
CGACCGCGAGAGCAGCCCGCGGGCGGCTACGACGGCAGCGACCGCGCCGCTTCGCGCGCGCGCGCGCT
CTGCTGCTGCTCGGCCCTTGCCCGCGCGCAGCTTTTGCGCCGCGACGCGCGCCCGCGCGCCCGCGCGCTGACGTGA
CCCTGTCCTTGGGCGGGGCGAGGACGAGTGGTCCGCGCGGGACGCTACCCGACGGCTGGCCCTGTGTGCTC
CTGGCAGTGAACCTTGGCGGGGTGGAGCGCCAGGCGAGCCCTCGAGGACCCCTGATTATTACGGGACGAGAT
CTGGAGCGGGGAGCTTACTACGGCGCGGGAGCCGAGCTCGAGACCTTCTCTCGCGCGCTGCTCTGGGGGCG
CGGGGGAGGAGTGGAGCGCGCGCGCGGACCGGCGCCAGGCGCAACCGGCGCAACCGGCAAGAGCTCCC
AAGAGGAGAGTGGCTCGGCGCGGCTCCACGAGGTAAACAGCAAGCAAAAAGTTATGAGAACAAG
CTCTGAGAAGGCTGCCACGATGATCAGAGTGTCTGGTGTGGCCCGTGAAGATGTTCAGAGAGATTTGCCACCT
TTGGTCTGGAACCTTAAATACAGACTTCAGCTCATCGTCCACGCGTGAAGCGATTTGGCTCTGGGGGCA
CATCGAGGAGATCAACATCAGGCGGGCGATTGAATAAATGATTTATGACGAGCGTGGTGGCGGGGAAG
AATGACCTCAGACGTGAATTAAGTGGATGCTGGCGCGCTACGAGATCATGGTGTCTCATCTCAAGGA
GGAATCTCCCTCTGGCTGAGTGATGGTGCATTAAGTCTTAAGTCTACCGCGCGGACGAGATGACCACCT
ACTCTTGAAGATGGATCGAGACATGATATTGAGGAAACAGTGAAGGAGATCCCTGTCTCAATGAGT
ACCGCTCCCATGTGGCGCGCTACATCCGATAAACCTCAGTCTGATTTATCGCGCGGACGAGATGACCACCT
GAATGAGATCTGGGCTGCCCTCCAGATCTAATAATTATTCACCGCGGACGAGATGACCACCT
GATGACCTGGATTTTAAGCACCAATTATAGGAATCGGCCAGTTGTGAAGATTTGTGAATGAATGTGTCC
CAATATCCACCAAGATTACACATTTGAAAAGAGCCACCGGCGGCTGAAGTCTGATGCTGTGAAGATCTCAGAT
ACCTGGGAGCAGTAAGTCTGGAGCGCGAGTTTCACTACATCGCGGGGCGCAACCGGCAATGAGGTCTGGGC
CGGGAGCTGCTGCTGTGCTGTGGTCAGTTCTGTGTCTCAGGATGACTTGGCCGGGAATCGGCGCATCTGCCACT
GTTGGAGGAGAGCGGATTCAGTCTCCCTCCCTCCACCCGAGCTGACGAGAGGCTACGAAGGGGCT
CGAGCTGGGAGGCTGTCTCTGGGACCTGGAGCCACGATGAGATTCGATCAACAACCACTTCTCTGATTTA
ACAACGCTGCTGGGAGGAGAGATCGACAGAGTCCCGAGAAATTTCCCATCACTATTTCGAATCCC
TGAGTTGTTTCTCTGGCAAAATGCGACGGTGGTCGCGACGAGCAGCTACATGCTGGATGGAAAAAATCT
TGTTGCTCTGGCGGCAATCTCAGGGCGGCGAGCTGTGTGGTGGCATTCCTACAGACCTGTGTGGCTCCCC
TGAAGACGCGAGGAACACCCCCACCCCGATGACGAGCTGTCTCCGCTGGCTCGGCACTCTCTTCTGCTCCAC
ACACCGCTCTCATGACAGCGCCGGAGGAGGGTGTGCCACGAGGACTTCGCAAGGAGGAGGAGGACATGTCA
ATGGGGCTCTGGCACAGCTCGCTGGAATGCTTGAAACATTTACGATCTTCATTCATAAAGCTCTCGAAGT
TCATCTACGTGGGCTGTGATAAATACCACTGACGAGCGAGTCCCGGAGGATGGGAGAAATACCGGGAATC
TCTGATCTGTTCATGAGCAGGTTTCATCTGTGGGATTAAGGCTTGTGAGAGATTCGATGAAAGAAATCC
CAACGCAATTTCTCCGTAGAAGCATTAACATGACATCGCAAGCAACAGTGGAGATCTATGGCGGCTC
CTGAACCTTGGAGAGTATGTGTTCAACGAGAAAGCGGAAGTTTCACTGATCCACCAAGAACTGTATGTTGTG
CTATGACATGGGAGGCCAAGTGTGATCTCACATTCGCAAAACCAATGCGCAGGATCCGAGAGATCATGG
AGAATTTGGGAGACGCGCTCGACCTCGCCACGAGCGGCTGAAGCTCGGGGCGGAGAGACGACAGCT
GGTGAACCTCTGGCGCCTTGAGACTCTGGGACCATGAAATTAACCAACCTGTGATGAGTCTCAT
TGACATGCTCACTGTCTTCTCTCTGTAATTAAGAAGTGCCTGGAAGAGGGTGCATTTGAGGACGAGTCC
CAAAAGGAAGGCTGGAGCTGAGGCTGTTTCTTTCTTGTCCCAATTTACCAANAATCTTGAGACAGCA
CGACAGAAAGCTGATGGAGTGAGAGAACTCAGCAAGCAACCTGGGAATCAGAGAGAGGAGAGGAGG
GCGCTGCTCGCTCGAGCGCTCGGCTGCATAGAAAGAGATTTCTGTGCTTCCCTGTTTGGTGGCAGCAAGG
GTTCCACGTGCATTGTCAATTGTGCACAGTAAATTCAGCATTTCCCGAGCTGGGCTGCCAATTTGTACCA
TTTGAAGTCTCCCGAGCGTCTTAAGAGAACTACCCCTCTCTGGCCCTGGGACATCGAAGCTCTGCAAAATA
ATTCTGTGTTCTTTGACAAATAGGCTCATGCAAAATGACATCAGTAGCGCTTGAATCTGTTTGTGCTCT
TTTCAACAAGAGGATGTGTTCAGAAAGGAGAGAGGAGCTGAGATCATCGAGGTTTGTGGGCGACAGCA
TGAGCTCTTCTGCAAAATTTGGGTCTATAAACCAACCCAAAGTCCCTGCTGATCAGTAGCCCTCGAGGTT
CCCCGAGTGGGAGCGAGAGTGGCGGACCTCTTGAAGGCGCGAGAAATTTAGCTCTGATCTCTCTTTTATC
TGCTAGGACTGGAAGAGCGAGAGTGGGTGGCTGAGGCCCTCTCTGCTGTGAGTATGGCCGCTGTGTG
GAATTGAGTGTCTATGGTTGSCCTCATATCAGCTTGGGAGTTATTTTGTGATGTAGAATGCGACATCTCCA
GATTAGGCTTAATGATTAAGAAACCTCTTAGATTATCTGTGTGAGCATGATTTGGGAGAAATTTGAATTA
CTCTGCAAGAAAAAGTATGCTCATCTTTTGTATTTGTTGCTGCTCATTGACCTGGGAAAAATGAAAAA
AATAAAGCAATAGGTAGACCTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGAALEDPDYYGQEIWSREFYYARPEPELETFSPLP
AGPGEWEERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVNVNEMCPNITRIYNIQKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGDIDNNNFPDLNTLLWEAEDRONVPRKVPNHYYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSFWKTQEHTPTPDDHVFRWLAYSYST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVMEQVHRGIKGLVRDSHGKGPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRQRQ

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FIGURE 37

CTAAGAGGACAAGATGAGGCCCGGCTCTCATTTCTCCTAGCCCTTCTGTCTTCTTCTTGGCCAAGCTCGAGGGG
 ATTTGGGGGATGTGGGACCTTCAATTTCCAGCCCGGGCTTCAGCTCTTTCCAGGTGTGGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTGGGGCTCCAGCTCCAGCCCGAGCTTAGCCAGCGGGAGTTCTGTGTCCTCAAGTTGTT
 TTCCAAATTTACCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTCTGTGTTTCCCTGCCAGACACCACTTTTC
 CCGTGGACAGAGTGGAAACCTTGGAAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAAGAAGAACTTTCTAA
 GTGAGGGAATATGTCCAATTAATAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT
 GGAGAAGGATACCAATTTCTTACACTGAACTGGAATTCAGCTGATCAAGGTAGAAATGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTTGACCACTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTCGTAGAGAAGCTTGAGACACTAGACAAAAACATGTCCCTGCCATTCGCCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAAGTGTGAGGCCCTCAAAGATCAAAACACCCCTGTCGTCCACCTCTCCCACTC
 CAGGAGCTGTGGTTCATGTTGTTGTTGTTGAACATCAGCAACCGCTGTGGTTTCAGCTCACTGGAGAGGGTTT
 TCTTATCTATATGTTGCTTGGGGTAGGGATTACTCTCCCGAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAAACACTGGATGATTGCTATTGTATATAA
 ATGTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAAACAAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTTATCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTTCATGGTATGTGGGTTCT
 GTATGCCACCCGTACTATGAACACCAGAACAGAAAGAGATTTTACTATTATGACACAAACACAGGAAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACATAAACCTTTTGACAGAAA
 CTTTATGCTATAACGATGGTACCTTCTGAATTAATGATCTTTCTGCTCTGCAGAAGCCCAAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTTGGTGAATAATAGTCTTCCACTTACTTAGATATCTCAGGGGGTGT
 CTAAAGTGTGTTCAATTTGCAGCAATGTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGCTCT
 TGATTTGGTGAAGTCTCTTGGGAATCATCTGCCCTCTCAGGCCGATTTTGCAATAAAGTCTCTAGGGGTGGGA
 TTGTGAGAGTCTAGGGGCACGTGGGGCTTAGTGAAGCTTACTGTGAGGAGGCTTCACTAGAAGCCCTTAATATTA
 GGAATTAAGGAACTTAAACTCAGTATGGCTCTAGGAGTCTTTGTACAGGAAATATTGCCAATGACTAGTCT
 CTCATCCATGTAGCACCACATAATCTTCCATGCTGCTGAAGAAACCTGGGGACTTAGTATAGGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAAACTCTCAACTTTTTTTCCCTCACTAGCAGCTGGAAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGTGCTGAGTTTATGGAGAGAGCCCTTTTT
 ATGCATTAAATTTGATACGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTTCTC
 ATTGTCCACCTTACTAAAGTCAGTAGAATCTTCTACCTCATAACTCTCTCAAAGGCAGCTCAGAAAGATTAG
 AACCAGACTTACTAACCAATTCACCCCCACCAACCCCTTCTACTGCCACTTTAAAAAATAATAGTCTT
 CTATGGAAGTCTAAGAAATGAAAAATTAATTTTCTTAAATTCATTATGGACTTTTATTTACATGACTCTA
 AGACTATAAGAAATCTGATGGCAATGACAAAGTCTAGCATTATTGTTATCTAATAAAGACCTTGGAGCATA
 TGTGCACTTATAGGTGATCAGTTGTTGCACTGTAATTTTTGCCCTTTGTTTAAAGCCTGGAACCTGTAAGAAAAAT
 GAAAAATTTAAATTTTTTTTCTAGGACGAGCTATGAAAAAGCTATTGAGAGTATCTAGTTATCATGTCAGATGTT
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTGAAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAAATGAT
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSSFPBGVDSSSSSFSSSSSRGSSSSSRSLGS
GGSVSQLFNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTFGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQHPNKGLYWVAPLNTDGRLLLEYRYLYNTLD
DLLLYINARELRITYGGSGTAVYNNMYNNMYNTGNIARVNLTNTIAVTQTLNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLYATRMTMNRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

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FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCCTCTTGTGACGTTGTGGAGATGGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCACTTGTGTGGAGAGTGCCTGCTTTGCTATGCCGATGCTGTCCTAGTGGAAAC
 AACTTAATCTGTAACTAGATGTATGCTATGCACTTTTCTTGCTTGTGGAGATATGCTAGCTTG
 TGTAAATGTTGATACCCAGGAATGGAAGAACACTGAATAAGATTCTGGATTTGTGAGAATG
 AGAAAGGTGTGTGCTCTGTAAACATTTGCTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTTCTCTCTTTTACTAATGATCAAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTTGGTCTTTAAATTTGCTGCAGCAATTGCAATTA
 TTATTGGGGCATTCTTCATTCCAGAGGAACTTTTACAACCTGTGTGGTTTATGTAGCAGTATG
 GCAGGTGCCCTTTTCTTCACTCTCATACAACCTAGTCTTACTTATTTTGCACATTCTATG
 GAATGAATCGTGGGTTGAAAATAATGGAGAAGGAACTGAGATGTGTATGCAAGCTTTGT
 TATCAGCTACAGCTCTGCAATTTATCTGCTCTTTAGTTGCTATCGTCCCTGTTCTTGTCTAC
 TACACTCATCCAGCCAGTTGTTGAGAAAACAAGGCGTTTCACTAGTGTCAACATGCTCTCTG
 CTTTGGTGTCTTCTGTAATGTCTATACTGCAAAAATCCAAGAACTCACAACCAAGATCTGGTT
 TGTACAGTCTCAGTAATTACAGTCTACACAATGTATTGCAATGGTCACTATGACCAAT
 GAACCAAGAAACAATGCAACCCAAGTCTACTAAGCATAAATGGCTACAATAACAACAGCAC
 TGTCCCAAAGGAAGGGCAGTCCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACATAATTC
 TCTTTTGTGTGTATTTTATCCAGCATCCGCTACTTCAACAAATAGTCAGGTTTAATAAA
 CTGACTCTAACACAGTATGAATCTACATTAATAGAAGATGTGGAGCTAGAAGTGTATGATG
 ACTGAGGATGGGGAGCATGTTTACCAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATTCTTCTTTCATCTTATGCTTTTCTTGCTTCACTTTATATCATGATGACCCCTACC
 AACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAGTCAAGTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTGTATGTTTGGACACTCGTGGCAGCCACTTGTTC
 TTACAAATCGTGAATTTGACCTAGTGTGAGACTTCTAGCATGAAAGTCCCACTTTGATTTATGCT
 TTATTTGAAAACAGTATTTCCAACTTTTGTAAAGTTGTGTATGTTTGTCTTCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATAGATTTTACTGCTTGTCTATTTTGTATTTTCTTACCA
 ATGCTTGTATATGTAAGTAGAATGAATTTGCAAGGAAAGTTTATGAATATGGTGAAGT
 TAGTAAAGATGGCCATTATTTGGGCTTATTCTCTGCTCTATAGTTGTGAATGAAGAGTAA
 ACAAAATTTGTTGACTATTTTAAATTTATATATAGACCTTAAGCTGTTTGAACAAATCTTATA
 GCAAATGTATGGCTGCCCTTTGAAATATTGATGTGTTGGCTGGCAGGATAGTGCAAAGAAC
 ATGGTTTATTTTAAATTTTATAAACAAGTCACTTAAATGCCAGTTGTCTGAAAATCTTATA
 AGGTTTACCCTTGATACCGAATTTACACAGGTAGGGAGTGTATTAGTGGACAATAGTGTAGG
 TTAGTATGGAGGTGTGCGTACTAAATGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAAGTGTTTTGGTGTGTTTAAACTCATGAAGTATGGGTTTCAGT
 GGAATGTTTGGAACTCTGAAGGATTAGACAAGGTTTGAAGAAGATATCATGGTTAGAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTTAGTTTGGGCCCAGCACGGTAGCTCAACCTT
 GGTAAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGGCCCCAGGAATTCAGACCA
 GCTTGGCACAATGGTGAACCTGTCTATAAAAAATAATCTGGCTTTGAGCATATGCCTTGGTCT
 CAGCATGAGAGCTAGTGAAGATTGCTGAGCCCAGAGCCAAAGGTTGCAGTGAAGCAAGTCA
 CGTCACTGCACTCTAGCTTGGCCAGAGTAAAGCCAAAAAATATATATATGAAATCAAGG
 AGGCAAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTTACTAT
 ATAAATCTAGTCAGTCTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTTCTCTGTACATTTAA
 AAATAATTTCTATTCAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAAATGT
 GATGTGGATTGCTGTGCTCCAGCATGACCCATAAACAGGTGAGAAGATGAGGAATGTTT
 AGAATAAAGTCTGCTTATAGTATACACAGTTTCAAAAGATGTTTAAATGCTTTTGTAT
 TTTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTTGAAGATCAAGCAGT
 ATGAGAGTTTAGTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTCAACAT
 TCTTTTAAAAATTTTATTAATGTGAATGGAATATAACAAATCAGCTTAATTTCCCAACC
 TTATTCTGTGTGATAGCATTGTATTCCACAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPVPCNILVGKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVKNLTLTSDSTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYSFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

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FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAAC TGAATAAGATTCC TGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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GTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTCCCCGTGTTGNTATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTGCTTGTGTGGAGTANGTGAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTTGGTTTG
GCTANGTTCTATNTTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCGAGTGACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCGTGT
TGCTATGCCGATGCTGTCTAGTGGAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGTT
CTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACTAGT
CTTACTTATTGATTTTGCACATTGATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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FIGURE 46

CTCGGGCGCGCACAGGCGAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTTCGCGGCCGGCGCGGCTCTCCAAT
 GGCNAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTCGGCAAGGCGAGTCGAGTGTGTTGCGAGACGGGGCGAG
 TCCTGTGAAAGCAGATTAAGAGAAACATTATTAACTGTCTATTACGAGGGAGAGCGCCCGCGGGCTGTCCG
 ACTCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAGAAAGCGGAAGAGGACGAGCATTCAC
 GTGCTTTCCAGCGAAGTGACCTGATCGATGGCCCTCTCGAATTTATCACGATATTTGATTTATTAGCGATGCC
 CCTGTGTTTGTGTGTACGACACACACGTCACACAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC
 TGGCGAATCCACATCTGTTTCACTCTCCGCGAGGGCGAGCAGGAGCGAGAGTGTGTGGAATCTGCGAGT
 AAGAGGGACGAGGGAAGAAAGAAACAAAGCCACAGACGCACTTGAGACTCCCGCATCCCAAAAGAGCAACGAT
 CAGCAAAAAAAGAGATGGGCCCCCCGAGCCTCGTGCTGTGCTTGTGTCGCAACTGTGTTCTCCCTGCTGGG
 TGGAGCTCGGCTTCTGTCGCAACCCGCTGAAAGGCGAGTTTCAGAGGGACCGCAGGAACATCCGCCCCA
 ACATCATCTGTGTGCTGACGAGCAGCAGGATGTGAGCTGGGTTCATGCAAGTGATGAACAAGACCGCGGC
 ATCATGGAGCAGGGCGGGCGCACTTCATCAACGCTTCGTGACCAACCATGTGCTGCCCTCAGCTCCTCT
 CATCTCCTGCAAGTACGTCACAAACCAACACTACACCAACATGAGAACTGCTCCTGCCCTCCTGCG
 AGGCACAGCAGAGAGCCGCACTTTGCCGTGTAACCTCAATAGCACTGGCTACCGGACAGCTTTCTCGGGAAG
 TATCTTAATGAATCAACGGCTCTACGTGCCACCCGCTGGAAGGAGTGGTGGACTCCTTAAAACTCCCG
 CATTATTAACACAGCTGTGTGCGAAGCGGCTGAAAGAGAGCAGCGCTCCGACTCTCAAGGATTAACCTCA
 CAGACTCATCAACATCAGAGCTGAGCTTCTTCCGACGTCGAAGAGATGTACCCGACAGGCGAGCTCCT
 ATGTGTCATCAGCCTGAGCGCCCGCCAGCGCTGAGGATTCAGCGCCACAAATTTACGCGCTCTTCCCAAACGC
 ATCTCAGCAGCTACGCGGAGCTACAACTACGCGCCCAACCCGCAACAACTGATCATGCGCTACACGGGGC
 CCATGAGGCCATCCATGGAATTCACCAACTGCTCAGCGGAAGCGCTGACAGCCTCATGTCCGTTGGAC
 GACTCCATGGAGCACTTACAACTGCTGTTGAGACGGGCGAGCTGGACAACACGATCATGTATACACCGC
 CCACCTGGCTTACCACTCGGCCAGTTTGGCCTGTTGAAAGGGAATTCGATATGATTTGACATCAGGG
 TCCGCTTCTACGTGAGGGGCCCAAGCTGGAAGCGGCTGTCTGAATCCCCACTGCTCCTCAACATTTGACCTG
 GCCCCCACTCTGGAATCTCAGGCTGGACATACCTGCGGATATGCGGAGGAAATCCATCCTCAAGCTCTG
 GGACAGCGAGCGCGCTGTAATCGTTTCACTTGAAAGAAAGATGAGGCTGTGGCGGAGCTCCTTCTTGTGCT
 AGAGAGCCAGCTGTACACAAGAGAGACATGACAGGTGGACGCTCCGCTGGCGGACAGCACTTTTCCCAAGTAC
 CAGCGTGTGAAGACTGTGTACGCTGCTGAGTACCAAGCGGCTGTGAGCAGCTGGGACAGAAGTGGCAGT
 GTGTGAGGAGCGCCACGGGAGCTGGAAGCTGCATAAGTGCAGGGCCCTTCCGCTGGCGGACAGCAGGCTC
 TCTCAACCTCTGTGCCCACTACTACGGCAGGCGAGCGCTGCACTGTGACACGGGGGACATAAGCTC
 AGCTTGGCGGACGCGCGGAAAAAATCTTCAAGAAGATACAAGGCGCACTATGTCCGAGTCTGCTCCTCGC
 CTCAAGTGGCCATCGAGTGGACGGCAGGCTGTACCACTAGCAGATGTGGGACTTCACTGAGGACTGTGAGG
 CTTCCGACTACTCAGCGCCCAACCCCATTAAGTGAACATCGTCTGCTACATCTAGAGAAGCAGACAGTCCA
 GTGTGACCTGGACCTGTACAGTCCCTGCGAGGCTGGAAAGACCACTGAGTGCATCGACACGAGGATTTGAA
 CCTTCAGAACAAATTAAGAACTGAGGGAAGTCCGAGTCACTTGAAGAAAGCGGCCAGAGAAGTTGAC
 GTGCACAAATCAGCTACCAACCCAGCACAAGGCGGCTCAGCAGCAGAGGCTCCAGTCTGCACTCTTTCAG
 GAAGGGCTGCAAGAGAGACAGGTGTGGCTGTTGGCGGAGCAGAGCGCAAGAGAACTCCGCAAGCTGC
 TCAAGCGGCTGCAAGAACACAGCAGCTGCAGCATGCCAGGCTCAGCTGCTTCCACCCAGCAACACGACCTGG
 CAGACGCGCCTTTCTGGAACACTGGGGCTTTCTGTGCTGCACCGGCAACAAATACACGACTCTGGTGCAT
 GAGGACCATCAATGAGACTCAAAATTTCTCTCTGTGAATTTGCAACTGGCTTCTAGAGTCTTTGATCTCA
 ACACAGCATCTACAGCTGATGAATGCAAGTGAACACTGGACAGGAGTTCCTCAACAGCTACAGCTACAG
 CTCATGGAGCTGAGGAGCTGCAAGGTTTACAAGCAGTGAACCCCGGACTGCAACACATGGACTGGATGGAG
 AAGCTATGAGCAATACAGGCACTTTCAGCTCGAAGTGGCCAGAAATGAAGAGACCTTTTCCAACTCATGG
 GACAACCTGGGAAGGCTGGGAAGTTTAAAGAAACACAGAGGTGGACTCCAAAAACATAGAGGACACCTCA
 CTGACAGGCAATGAAGAACTGTGGGTGATTTCCAGAGCACTGTGCTATTGGCCAGGAGGCTGAGAAAG
 AAGCAGGCACTTCAGTCAACATCAGAGATTCGGAGGATAACAGCAGGAGCAGAGATTAACCTCAGGAACTCC
 ATTTTGTGCCCTGCTTTTGTGATTATACTCAGCACTGACAAATGCAATTTTTCGATCAAAAGTCC
 ACCATTAACCTCCCCAGAGCTCACAAGGAAACGGAGAGAGCAGCGAGCAGAGAGATTTCTTGGAAATTTT
 TCCCAAGGGGAGAAAGTCTGGAATTTTAAATCATAGGGGAAAGCAGTCTGTGTTCTAAATCCTCTATTCTT
 TTGTTTGTGACAAAGAGGAACTAAGAGCAGGACAGAGGCAACGTTGGAGGCTGAAACAGCTGACAGAGC
 TTTGACATCAGTCACTGACCAAAAGAGATGACATTTTACCTAGCACTATAAAGCCTGGTGTGCTCTGAAGAA
 CTGCGCTCATTTATATATGTGACTATTACATGTATCAACATGGGAACCTTTAGGGGAACTATAAGAAAT
 CCAATTTTCAGAGTGGTGTGTAATAAGCCTCTGTGGCCAGTGTAAAGAAAAA

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FIGURE 47

MGPPSLVLCCLLSATVFSLLGGSSAFLSHHRLKGRFQDRDRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP
SYNYAPNPDKHWMRYTGPMKEPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEFDIRVPFVYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKKDKVLLREQKRKKLRLKLLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNTYWCRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNLTDRDVLNQL
HVQLMELRSCKGYQCNPRTNRMDLDGGSYEYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

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FIGURE 48

AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTTCACC
 ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
 CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
 CGCTCGCTGAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
 ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
 ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
 GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCCGGTGCCTTAGTCCAAGAAAAT
 AAAAACCCTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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FIGURE 50

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCAAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCG
 TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAAGCTTGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGTGCCACACTGTACCTGGGGCAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTCCTCCTTCTCTGGGGAGGAGGGGTTCTTGAGGGACCTGACTTCCCCTGC
 TCCAGGCCCTTTGTCAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCGAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGAGGACTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAAA
 AAAAAAAAAA

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FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCVGSILSEGEESPSELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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CCGCGGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCCCTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCTGTGTGGAGCCCCAGAACCATGTGCCAGCCGCTGCTTTTGGA
GACACGCTTCACTATACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCCTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAAACGGGGATTTCACCATTCTGTCCAGCGGATGCGAGTGGTGCAGTATTGCGCTGGAGT
GATTGCACTAATCCGAGCCAACACTATGGCTAAAGTGTGAGAAGGCATTTGCGCTGTGGTAG
GGATGGCCATGTGTCCAGCCCTCTGGGCTCAATGGGTATCACTTACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**ATA**
ATAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

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FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAATTTAAAAAACTTA

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FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

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FIGURE 56

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT
 ATAAAAATGTTAGAGGAACTTTACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAATAATAAAGAAATTACAAAAGAAATTATGGATTGTGCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCGGTGG
 TCAAAATCTTCCCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCGGTGGGATGCACAGTCACTC
 CACATCCACCCTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATG TTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTGTTTGGGTCAAACAGGTGCTCGCATTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAGACATAGTATACCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCGTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTGTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCCTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCGGCGGT**ATG**TGGCTTCGCTGGTGTCTCTGGCTGTGCTGCTGCTGGCGGTCC
TCTGCAAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCCAGCGCCCTGGTAAC TGACAAGGAGGCCAGGAAGGTTCTCAAAACAAGC
TTTTTCAGCCAAGCAAGTCCCGGAGAAGCTGGATGTGGTAAATTCGACAGTGGCTTTGGGG
GCCTGGCTGACCTGCAATTCTAGCTAAAGCTGGCAAGTGAAGTCTGGACACAGGAAT
ACCAAGGACAGGGGGCTGCTGTCTACCTTTTGGAAAGAAATGGCTTTGAATTTGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGCGACATTTGGCGGTTTATCTTGGACACAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCTGTCTCTCTCTTTTACACATCATGGTACTCGAAGGGCCC
AATGGCCGAAGAGGATACCCCATGTACAGTGGAGAGAGCCACATTCAGGGGCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGATATATAAGCTGGTTAAGTGGGTATCCA
GTGGAGCCCCCTCATGCCATCTCTGTTGAAATTCCTCCCATGCCCCGGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACAGAGATCTGGCTGA
GGTCTCTGCAGCAGCTGGGGGCTCTCTGAGCTCCAGGCAGTACAGCTAGCATCTTCCCCA
CTTACGGTGTCACCCCAACACAGTGCCTTTTCCATGCAAGCCCTGCTGTGCTCAACACTAC
ATGAAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTTGCTTTCCACACCATCCTCTGT
GATTACAGGGGCTGGGGGCGCTGTCTCTCAAAAGGCGACTGTGCTAGAGTGTGTTGCTGGAGT
CAGCTGGGAAAGCTGTGGTGTCTAGTGTGAAGAAGGGGCACTGAGCTGGTGAACATCTATTTCG
CCCATCGTGGTCTTCCACAGGAGCTGTTCAACACCTATGAACACCTACTGGCGGGGAACGC
CCGCTGCTGCCAGGAGTGAAGCAGCAACTGGGGACGGTGC GGCCCGGCTTAGGCATGACCT
CTGTTTTCTATCTGCGCTGCGAGGCACCAAGGAAGACCTGCACTGCGCTCACCAACTACTAT
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTTCTCATGCGCCAGGGAAGA
GGCTGCGGAACACCATCCCTTCTCTTCTTCTGCTTTCCCATCAGCCAAAGATCCGAGTGGG
AGGACCGATTCCAGGCCGCTCCACCATGATCATGCTACATCCCATGCTGCTACGAGTGGTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCACTGACTGATGAGACCTTCAAAGACTC
CTTTGTGGAAGCCTCATGTCTAGTGGTCTGAAACTGTTCACACAGTGGAGGGGAAGGTGC
AGAGTGTGACTGCAAGGATCCCCACTCACCAACAGTTCTATCTGGCTGCTCCCCAGGTGGC
TGCTACGGGGCTGACCATGACCTGGCGCGCTGCAACCTTGTTGATAGGCTCTTGAAGGC
CCAGAGCCCCATCCCCAACCTCTATCTGAAGGCCAGGATATCTTCACTGTGGACTGGTGC
GGGCGCTGCAAGGTGCCCTGCTGTGTCAGCAGCGCCATCTGAAGGGCACTTGAAGGCACTGATCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAGAAGAAAGAAAT**TAG**TTCCATCAGGGAG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTCTG
CATTAAGTTCTTGCACGTATAAAGCACTCTAATTTGGTTCTGATGCTGAAGAGAGGCTAG
TTTAAATACAATTCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTCACTTGGATAGCTTTGATG
TCTCATGACGAGCGGGCGCTCTGCTCATCCCTCACCATGCTCTCTAATCACTGATGATCAAAGGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGACGTCAACCTGGTGGGTTCAGTTG
TGTCTTGAGGCTTCTGCTCTATTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACCTCAAACCTGGGCGTGGTTTTGGTTGCCATTTCCATA
GGTTTGGAGGCTCTAGATCTCTTTTGTGCTGGTTCAGTGGCTTCTCAGGGGACAGGAATA
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGTAAACAGCAGGATTCATCAGTTAGTA
GGGTGCATGTCAGATGATCATATCCAATTCATATGGAAGTCCCGGGCTGTCTCTCTTATCA
TCGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGAGCTAGTACTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGAAGGTTGATGAGGGAAGGTTGACATCAGGACTCAGGGA
TGGACTGGTAAAGATGAATCACTTTGCTGGGTGAAGCAGGCTGCAGGCTATCCAGCCAAAGG
CACAGCAGGAGCAGTGCAGGAGGTTGTGGGGTAAGGGGAGGATCATCATAGAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCCAGAAATGGCATTTGCACTTAATAGACATGTGAGG
TAGACAGGTAGGTGAATGCAAGTTTGAAGAAATGACTTTTTCAGTTATGTCTTATG
GTATCAGACATACGAAAGGTTCTTTGTAGTTCGTGTTAATGTAACATTATAAAATTTATTG
ATTCCATTGCTTTAAAAA

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FIGURE 64

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDKRPPAPLVTDKARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYYVYDMDQAMERYVSMPEEAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDGLRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRI RAQKKKN

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FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGGTGTCTGCTGAGCTTGGCCTCGGCGTCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAACTCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTCTAG
 AGTCTCCAAATCCAGAAAAACAAGGACTATGAAGAGCCAAGAAAGTACGGAAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGAGGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAATGGAATGAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTCTATGCTCTTTTATTGGTGATTACTTGCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAGTCAGGCAGGCTCTTGTAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTT
 TCAGCTTTCATGATCCAGATTTGCTTGATTAAGACCAAATATTCAGTTGAACCTCCTTCAA
 ATCTCTTGTTAATGGATATAACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA
 ATTTTTCTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTAAATTTTCTCTGAGTTGGAATTGTGAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAGAAATGACTCCAGAGAGCTCTACTTTCTGTTTTTTACTTTTCATGATTGGCTGTCTTC
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTTGCTAATTTGGAAGATTAACTCATTTTAAATAAA
 ATTATGCTAAGATTAAAAA
 AA
 AA

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FIGURE 66

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SEESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
EPCHFPPFLFLDKEYDECTSDGREDEGRLWCATTYDYKADEKWGFCETEEEEAAKRRMQEAEEM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLFPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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CTTCCCAGCCCTGTGCCCAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCTTCTGATGGGGACCTTCCT
GTCAGTTTCCAGACAGTCTTGCCCAAGCTGGATGCACTGCTGGTCTTCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCCTCGGAGGAGGATCA
CCACCGGCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT
GTGTCTCACCATTAGTCCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCCTCCCTCTGCCTCCCATTTCT
GCCCCGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCCTGTGAAAATGGG
TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

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FIGURE 69

GCGCGCCCGCCCGAGACCGGGGCCGGGGCGCGGGGCGCGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGGAGCGACGCGCGGGGCCCGCCCTGACCCCGCGCGCGCGCCGCTGAGCCC
 CCGCGCGAGGTCGGACAGCGCCGAGATGACGACCGCGCGCGCGCGCCGAGGCCCCCAAGAGATGAGGGAC
 AAGGCTGGTCCGACGCGAGGTGGCCCGGCTGGGCGCGCACTGTGCGGCTGCACTGAGTGGCCAGTGGGA
 GGGGGACCCCGCGCGCTGACCATGTGGACCAAGGATGGCGGACCATCCACAGCGGCGTGGGA
 GCGCGCTTCGCGGTGCTGCGCGCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCGGCG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCGAGCCTTGAGCGTCAACTACACCTCGTCTGT
 GCTGGATGACATTAGCCCCAGGGAGGAGAGCCTGGGGCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCCGCGCAGCGAGGTGGGACGACGCCGCTTACACAGCGCCTCCAAGATGAGGCGG
 CGGTGTATGCAACGCGCGTGGGTAGCTCGTGGGGCTCAAGTGGCTGGCCAGCGGGGACCC
 TCGGCGCGACATCAGTGGATGAGGACGACCAAGGCTTGACGCGGCCAGAGGCGCGTGGAG
 CCGGAGAAGAAAGTGGACACTGAGCCTGAAGAACCTGCGGCGCGGAGGACAGCGGCAAAATAC
 ACCTGCGCGCTGTGGAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA
 GCGGACCCGCTTCCAAGCCGCTGCTCACAGGCACGACCCCGTGAACACGACGCGTGGACTTCG
 GGGGAGCCAGCTCTTCCAGTGAAGGTGCGCAGCGAGCTGAAGCGCGGTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGGCGCGAGGGCGGCCAACACTCCACCATCATGATGTGGGCGGCCAGAA
 GTTTGTGGTGTGCGCCACGGGCTGACGTGTGGTTCGCGGCGCGAGCGGCTCTTACTCAATAAAGC
 TGCTCATCACCCTGTCCGCGAGGACGATGCGGGCATGTACATCTGCTCTGGGCGCCAAACACT
 ATGGGCTACAGCTCCGAGCGCTTCCTCACTGCTGCTGCCAGACCCAAACAGCCGACGGGCG
 ACTGTGCGCCCTCTGTCTGCTGGCGCACTAGCTTGCCTGGCGCGGTGGTCTATCCGATATCCGAG
 CGGCGCTGTCTCATCTGCTGGCGCACTAGCTTGTGCTGGCTTTGGCAGGCCAGAGAAGAGCGG
 TGCACCCCGCGCGCTGCGCTCCCTGCTGCTGGCGACGCGCGCGGGGACGGCGCGGACCGG
 GTGCGGAGACAGGAGACTTCCCTCGTTGGCGCGCTCAGCGCTGGCGCTGGTGTGGGCGCT
 CAGGAGCATGGGTCTTCGCGGACGCGCCCGCACTTACTGGGCGCCAGGCGCCAGTTGCTGGC
 CCTAAGTTGTACCCCAAATCTTACACAGACATCCACACACACACACACACACTCTCACAC
 ACACCTCACAGTGGAGGGCAAGGTCCACACGACACATCCACTATCAGTGTGAGAGCGGACCGT
 ATCTGCACTGGGCGCGGGGGGCGCGCCAGAGCGAGCTGGGAGGATGGAGGACGGAGCT
 GCAGACGAAGCGAGGGGACCTTGGCGAGGAGGAATGGCCAGCACCCAGGCGAGTCTGTGTG
 TGAGCGATAGCCCTGGACACACACACAGACACACACACTTACCTGGATGCATGTATGAC
 ACACATGCGGCGACACGTGCTCCCTGAAGGACACGCTACGACACACGCACATGACACAGATATG
 CCGCTGGGCGACAGATAAAGCTGGCCAAATGACGACACACGACAGACATGCCAGAA
 TACAAGGACATGCTGCTGAACATACGACACGACACACACACACACACACTGCTGCTGGAC
 CACACACACACACAGATATGCTGCTGGACGACACAGCTGCAGATATGCTATCCGGACACA
 CAGCTGCACAGATATGCTGCTGGACACACAGATATGCTGCTGGACACACACACACACAGG
 ATATTGCTGGACACACACACACACACAGCGTGCACAGATATGCTGCTGGACACACACAGG
 ACATACAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACAGGCGCAGATATGCT
 GCTGGACACACAGATATGCTGCTAGTACACACACACAGCAGACATGCTGTCCGACAC
 ACACAGCATGCAGATATGCTGTCGGACACACACACGACAGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCTCAACACTACACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGCTGGACATGCACACAGTGCAGATATGCTGCTGGGACACACTCCGGA
 CAGCACACATGTCAGATATGCTGCTGGGACACACTTCCGACACACATGTCACACACAGT
 GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTCAACACTACACACAGTGCAGAT
 TATTGCTGGACACACACTGTGCACAGATATGCTGCTGGACACTACACACAGTGCAGATA
 TGTGTCGGGATACACACGACACGACACACTGCTGCTGGGACACAGTGCAGATATGCTGCTGGG
 CACACATGCACACAGGTCAGATATGCTGCTGGACACACGACAGCTGACGTGCTTTGG
 GAGGCTGTGCGGTGAAGCTGCTGCTGAGTACGCTGCTGCTGAGGCTCATAGTGTAGGAGCTTT
 CCGTGTCCACCGTCACTCCCCAACTCTGCCCGCTCTGTCCCCCGCTCAGTCCCCCGCTC
 CATCCCCGCTCTGTCCCCGCGCTTGGCGCTTATTTGGACACTGCTTTGGGTGGCCAGG
 AGTCCCCCTACTGCTGGGCTGGGGTGGGGGCGACAGCGCCCAAGCGTGAAGAGGCTGGAG
 CCGTGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGGCTTGGTA
 TTTTATTTTAAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGAGG
 GTGGTGTCTCTCTGGGCGCGGGACCGCGCTGGTCTTTCAGGCATGCTGATGACCAACCC
 GTCCAGGCCAGACACACCCCCACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA
 GTAGAGTTTGGAGTGAAGCCCGGTATATTTAATTTATTTTGTAAACAAAA

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FIGURE 70

MTSPSLLLLLLPPLLGAFFPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIAEPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL
TGTHPVNTTVDFGGTTSFQCKVRS DVKPV IQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSHSHVEGKV
HQHIHYQC

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FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCAGAGTCC
 AGTGACTCTGTGAAGCCCCACATCTACTCTTGGCCAGGTTCCACGGGCTTGGGGGAAAAGATGGTGGGGGACCA
 AGGCTGGGGTGTCTCTCTCTGGTCTGGAAGTCACATCTGTGTGGGAGACAGACGATGCTTCAACCAGTCA
 GTAAGAAGAGTCCAGCCTGGGAAGAAGAACCAGCATCTTTGCCAAGCCTGCCACACCTTGGAGAGCCCTGGT
 TGAGTGGACAACTGGTTCAACATCCGACTACCCAGCGGGAAGGCGCACTATGAGGCGCTGGAGCGCATTCGCT
 TCTACTATGGGACGCTCATGTGCGCGTCCCTCGGGAGGAGGCTCGGACCACTGACTGGACACTCGCGGC
 AGCACTCGGCGAGCGTCCATGTGATCTCCCGTGAGGGTTCTGTGCTCTCAAGGAGGAGCGGCTGGCA
 GAATCTGCTTAATACACCGTACGCTTCTCTGCCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGA
 GCCATGGTCTCCCTGGAGCAAGTGTCTAGCTGCTTGTGTCAGACTGGGTCCAGACTCGCACACGCATTTGC
 TTGGCAGAGATGTGTCTGCTGTGAGTGAGGCCAGGGAAGGAGGTCAGCACTGCATGGGCGAGGACTGTACAGC
 CTGTGACCTGACCTGCCAATGGGCGAGTGAATGCTGACTGTATGCTGCTGATGTGGCCAGGACTTCATGCTTCT
 ATGGGGCTGTCTCCCTTCCGAGAGTGCTGAGGCTCGGAGCTGCTATCTACCTCTGACCAAGAGCCGGAAG
 CTGCTGACCCAGACAGCAGTATGGGAGATTCTGGAATCCCTGGCTTGTGCCCTGATGCCAATGCTGAA
 GATCAAAAGGTCAAGTTTGCCCCCATTTGATCTCACAAATGCCAAGACTAGCTGAAGGCGACCCATCAAGG
 CAGAGTTTGTGAGGGCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCAGGAGAGCTGGGCAGAGC
 GTGTCTCTGTGCTGAAGGCCACAGGGAAGGCCAGGCCAGGACAGCAAGTATTTTTGGTATCATTAATGACAACTTGT
 GGTCTTCCCTCTGAAGCATGAGAGCAAGCTGGTCTGAGGAACTCGAGCAGCAGCAGGCTGGGAGTACT
 TTTGCAAGGCCAGATGATGCTGGGCTGTGAAGTCCAGGTTGCCAGGCTGATTTGTACAGCATCTGATGAG
 ACTCCTTGCAACCCAGTCTCTGAGAGCTATTTATCCGCTGCCCATGATTCTCTCAAAATGCCCAACTC
 CTTCTACTATGACTGGGACGCTGCCCTGTTAAGACTTGTGCAGGCGAGCAGGATTAATGGATCAGGTGCGCTG
 ATGCTGTGCAAGACTGCTGTGGCATCTCAAGACAGGGAAGGAGAGTCCAGTGCAGTGGCTACACGCTACCC
 ACCAAGGTGGCCAAAGGTGCGAGCTGCCAGCGGTGATCGGAAACTCGGAGCACTGCTGGCGGCGCTGTCTAGTGC
 TCGTCAAGTGGGAGCCCATGCGCTTTGGCCATGTGTACATGGGGAACAGCGCTGTAAGCATGACTGGCTACA
 AGGSCATCTTACCTCTCTCTCCCGAGACTGAGAGGCTGTTGTCACATTTTGGACAGCTCGAGAAG
 TTTGTCAACCAACCAGAAAGTGCTACCTTTCAACAAAGAAGGGAGTGCCTGTGTTCCATGAATGACATGCTTCA
 CGGAAGAGGCCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTTGTTGAAGACC
 CACTGGCTGAACCTGGAGATTCCATCCAGGAGTTTCTACAGGCAGAAATGGGGAGGCCATACATAGGAAAAGTGAAG
 GCGCATGTGACCTTCTGGATCCCCGGAATATTTCCACAGCCACAGCTGCCAGACTGAOCTGAACCTTCATCAA
 TGCAGAGAGACACTTTCCCTCTCGGACATATGGCATGTTCTCTGCTGACTTCAGAGTGAAGTTCAGAGG
 AGCCACTTAATCTCGGCAAGTGAAGTCCAACTTTGACTCGACCACTCAAGTCCAGAGCAATATTCACAA
 GTGAACTCTGGTCTACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGTGAATCAAATTTGAAAATCAAAG
 GAGGAACAAAAGAGGAAGACAGAACTTCTGCTGGGCAACCTGGAGATTCGTGAGAGGAGGCTCTTTAACTCTG
 ATGTTCTCTGAAGCAGGCGGTGCTTGTGTTAAGGTGAGGCGCTTACGGAGTGTGAGAGGCTCTTGGCTAGTGACGAG
 ATCCAGGGGCTGTGATCTCCGATTAACTCTGGAGCTAGAACTGGCTTCTGTCCAAACCCATGGGCGCTGGGG
 CGCTTTGACAGTGTGATCTCCAGGCGCCAGCGGGCTGTGTGCTCTGCTTGTGATGACAGGCTCCGATGATG
 CTTACTCTGCTTATCTCTTGGCAAGCTGGCTGGGAGGAACTGCAAGCAGTGGATCTTCTCTTAATTCAC
 CCAATAGCAATTTGGCTGCTCCTCAGCCCTATCTCAACAACTCACTACGCTCGGAGCGGACCATGAGGATCCAG
 GGTTAAGAAAGACAGCTTTCCAGATTAGCATGGCCAGGCCAAGGCCCACTCAGCTGAGGAGAGCAATGGGCCCA
 TCTATGCTCTTGAGAAGCTCCGGGCATGTGAAGAGGCCACCGCCAGTGCAGGCCAGCTTCCGGTTCTACCGATT
 GAGGGGATCGATATGACTACACACAGTCCCTTCAACGAAGATGACCATATGAGCTGGACTGAGAGCATCTCT
 GCAATGTGGCCAAACCGCTGGAATTCAGGCGCTGCTATTCAGAGTGAAGTGTGTGGGCACTGGAAGTGA
 ATGTGGCATCGGCAACATGGGGGCACTCATCGCGGACAGTGGGAGCACTGTATGCAATCCGAGATCTGAGG
 AGCATCTGGGACAGGAGCAGCCCAATGTCTCAGCTGCTGTGGATTTCAAGTGCAGTGGATGCTCTATGA
 TCGAGGACCGTGTGGACCCGACCTGGTGAAGGTCTATCCCCAGGCGAGCTGCCCTCGAGCGAGTGTGAAGCCCA
 TGCTGCATGAGTACTGTGTCAACCACTTGGCCATTCGACTTCGACTCAACAAAGCAGCAGGATGAGTACACACTCTGGGA
 CCTTGGACACTCGGCAACACTATGGCATCTACACTGTCACTGACAGGACCCCTCGCAGCGCCCAAGGAAGT
 CGGCTCGGCGGCTTTGATGACCAATCCGATGCTCTTCAAGATCATCAAGCAATGTGGGATGAGTGGCC
 TCACCTTCAACTGTGTAGAGGAGCAAGTAGGCCGCCAGAGTGGCTCCAGTCACTCCCAAGACCCACCGCCAG
 TCCCTCTCGAGGCACTGTCCAAGGAAGAGTGGCTCGAGGCGGACAGGAGGCGAGGCGAGGGGTGGCCAGGC
 CAGGGTGGAGTGGTGGCTCTCTGAGATTTCTAGAGTTGCTCAACAGCCCTGATCAACTAAATTTTGGTGT
 ACTTACCGCTCTTCTGGCCCTATTTCATGTGACAGCATTTGAGACTGATGCAACAACTGTCACTTGGTTAAT
 TTAGCACTCTCTTCTGCTGATGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTGCT
 TTGGCAGTGGGCCCCCAATGGCAATATAGCCCTTTGGAACCTTTCTTAATGATTAAGACACAGAAAT
 GGCCACGTGTAATACTCTGAGCTTCACTGTACTTCAATTAAGGCAATTAATGCAAAATATACTTCTCTTCTT
 TTTGCTGATGGTTTGGCCACCTGCAAAATAGTATAATCTGTATGCTGCTGAAGATCAAAATACCAATATAAGCATAT
 TCTTGGCCCTTGTCTCCAGCAGGACATAGGCAAGCCTTGATCATAGTTTATACATATAAATGGTGGTGAATAAAG
 AATAAARCACTAATCTTTACTTTGAATTTGAATTAACCTATTATTCTTCTTGGTAAATTTGAATTTCTAGTGC
 ACATTAACCTTAAGCTTAATAATTAAGCTTCACTTCACTACAGTGTGGGAAGAGCAATCTCTGGT
 ATCCAAATTAACCAAGTGTGTAACCTGATTTGTACATTTCCCTTGCATTGCTTGTCTGCTAGAAAC
 CCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACCTGTATTTGAAAAA

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FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSFREGFWCLNREQ
 RPGQNC SNYTVRFLCPPGSLRRDTERIWS PWS PWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCMPGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVLTPMKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQONATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNC GISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPIYIGKV
 KASVTFLDP RNISTATAAQTDLNF INDEGDTFPLRTYGMFSVD FRDEV TSEPLNAGKV VHL
 DSTQVKMEPHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKV RAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVP AFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHDPR
 VKKTAFAQISMAKPRPN SAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPPFN
 EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV
 NNDS EYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACCTTTCATATTGGTTTGGGATCTGCTTTGAGGTCCTCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGATACGCATACATACATATGTATATATATGTAACATAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAAGAGATTACAAAGAAATTTAGAGATGATTTGTCAAGATCCCTGTCGATTCTG
 CCGTTTGGGTTACGGTGTCTCAGTGTGATGCAGCCCTACCTTTGGTTTGGGGACATTATGATTTGIGTAAGACT
 CAGATTTACACGGAAGAGGAAAGTTTGGGATTACATGGCTGCCAGCCGGAATCCACGGACATGACAAATTA
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTGTGGAGACCTCTGAGACGTTCTGTGCAATGGGCAATC
 CTTACATGTGCAATTAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGTCTGGAGCAAAACATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AATGATCCTGGAGAAGTCTCTCGATTATGGACGACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAAATCATTTCACACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTCACAGACTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCAAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGAAGTGCACAA
 ACAAGCTGCGCTGCTGTGCCCCGGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGCTGGC
 AGCTGCGGCTCCGACTCTGCGCAGGGCGCGCCCCGCAACGGCACCCAGCGCTGCTGCTGCTGACACGCTGCT
 GGGAAACGCCAGCCCTTGGTGTCTAGGTTGTACCTCCAGCCACACCGGACGGGCTGTGCGGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACAATAGGAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTTAAGTGAACATAAGCCATATTTATCACCCTGGACAGCACATCCAGTCAAGACTGTTAAATTC
 TGAATCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCAGATTGCCAGCTCAGAGCATATTGTTGGA
 TTGGAAGGCTGCGACAGCCCCCAACACGGAAGACAAAAACAACAAATCAACCGACTCAAAACATTTGGC
 TACTCTAGCTGGTGGCCCTAGTACGACTCCGCCAGTGTGGACCAACCAATAGCATTTCTTGTCTGTCAG
 GTGCATTGTGGGCATTAAGGAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTGCTCTGTAACCTCGTTGGTTGAAGATTTCTTTGCTGATGTTAGTGTAGTCACA
 TGTGTAACAGCCCTCTAAAAGCGCAAGCCAGTCTATACCTCTATATCTTAGCAGCACTGAGTCCAGTCGCA
 GCACACACCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTATCTATCCTTTTGATTTCAAATCAAGTT
 ATTTTCTTGAACACTCTGAATATGTAGATTTTTTGTATTATTGCGCAATTTGTTGTTACAGACATCTGTTAAAT
 GTATCTAATTCGAATCAGCAAAAGTACATTTTATTTTGCTCTTTCTGTTCTGTTTGTTCCTGTTGCGAGA
 GATTTCTCTGTAAGGGCAACGAACGTGCTGCGATCAAGAAATATCAGTTTACATATATAACAGTGTATTAAGA
 TTCCACAAAGGACATTTCAATGTTTTCTGTGTGCTTTAACACTGGGAAGATTAAAGAAATAAAACTCCGTGCA
 TAAACGATTTTCAGGAATTTGATGTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTTCACACTCACT
 TCTGATGTTCTGTGGACTGAGTACATTCAGCTGACAAATTTAGTTCCCGAAGATGGATTGATGTTCACT
 AGCTTGACACACTTCTGCAAAATATGAGACTATTCACACTTGGGAAAAATTACACAGCAAAAAA
 AAAAAA

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FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYFKPLQVNIITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRFWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

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FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGCGAGGCGCCGACTTCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTTGGACCATGTCGGTGATCTTTTTTGCCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTTCTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTC
 AGCAGCCATGGCCTTCTGCTTCTTGAGACCCCTGGTGGGAATTCACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGAAATCTCATCAGCAGGAGCCTGTGGA
 AAAGGGCATGTCAGTGAATCTGGGAATGGCTGGATTTCGAAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTGATCCCCCAGGATTCATTTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGTCTGTTTCATGTTACACAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGCGAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAA
 AAAAG

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FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEFAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAATAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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FIGURE 78

CTCAGCGGCGCTTCTCTGCTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGTTG
 CCGTCCCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGGTGGGTCTGGGTGCTTGGCGGCGCGGCTT
 CCTCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGTAC
 CCGCTTCAAGAAGCCTGCTGAGTTACCCACAGTGGATGATGAAGATGCCACCCTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCTGCTCGGAACCTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTCTCTCTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTGGTGGCTCCAGAAAG
 GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCTATCCTTCTCTGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTCTGGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCGATGCAAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCATTCAAGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGCACTGCCATGACGCAGATAATT
 GGGAACTGTGCTCTGCTCTCTCTGGTCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTCTCTACAACGCAGCCTTTGCAAGGCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGTGCCGT
 CTCCGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGACCTCCAGCTGGGGTGGA
 AGGAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGTTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATTT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCTGCTTTTCCATACTTAACTGTGGCCT
 CAGCATGGGTGAGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGTGAGGGGACGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTGTGCTCTGGCCAGCAGACGCTTAAGCACTGTGCTATCCTGGGCGGCTTTGGACCACTG
 AAAGACCAAGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVL SVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATV NK
IALELCTFTLAIALGAVLLL PFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGV LGRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLP LDMELLHRQVLALQTQ RVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSFSKLGSGFAVIQVVLI FYLMVSSVVGFY
SSPLFRSLRP RWHDTAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDGFRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTF TAAVRAELIRAFGLDRLPLPVSGFFQASRKTQH Q

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCAACACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCCTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGCTTCCT
CCCCGTTGTCNTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACCTGCAA
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCCCTCAGTAGCCCTGTGCACTTGGAATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAGAAGTACTCCAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTILTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAGAGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGTGGGCTGGCGAGCCGACGCGCGCGGAGGCTGTGAG
 GAGTGTGTGGAAACAGGACCCGGGACAGAGGAAC**ATG**GCTCCGAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCCGAACCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCTTAATGTCAAAGTGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCCAAATATTTGAAAGGAGAGGAGATGATT
 GTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCGAGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTGATGTGGATTTTCCAAAAGAACGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGA**GAGTG
 AATAAAATTTGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAGCTGCAAGGAGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATCAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTTATTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDCEPNVKLVNEERTLEVEIEPGVRDGMETPFIGEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGCGGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCCTNGAAGTGCCTTNTATAAAGGATATTAAGG
CCTATAGGAAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGAGGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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FIGURE 87

GGCACGAGGCGGGCGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGCTGTTGAGGAACTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGAGCC
 TTGGTGCTGGTTTGAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTACACTCTGAC
 AGAGAAGCTTGTGGCATGACAAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGCCAAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCTAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCTCTGCAGGAGCAGTCTGCAATTT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTCTTCAAGAAAATTGAGCCACCGTCT
 AAGAAAATCAAGAGGTTTCACATTAAATTTAGAATTTCTGGCCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTA CTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCCT
 GGTCCCTGAGGCGCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAAC
 ACAAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSA
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTCCGAGGTGCTTTCGCGCTGTCC
 CCACCACTGCAGCC**ATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTTCCCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTCAGAT
 TCTTCTTCCAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTTCAG
 GGGCTTCTTTCCTGTCGTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TA**ACAACA
 AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGTCACCTGCAATGGCAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

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FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

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FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGAAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTGAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCCTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGCAGGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCCTTCCTGAGTCCTGGATCTTTCTTCCTCTCGGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
 ATCAACACCATTACAGTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCAGCGAATGCACCATCTTACGGACCCGCGCCCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAATTTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT
 GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
 GACGCCCATGGTGCCCCCGGGCGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCCCTTCTTCCAGTTCCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCCTCGTCTTCTTGTGGCCTCCGTGGGAGTTGATGGATGATTGGTGT
 GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTCAACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAAGGATTTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGGACAAAGTTCCTTTCATCCTTTGGTGCTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTAAAAGTGCCTTTAGGTGAGATGACTAAATTTATGCCTC
 CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

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FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLWPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTFEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVWMIGVTEIDKGSAYGNSDS
KQKLND

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FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTTCAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGCTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGGCTGCTTCACAA
 AAACCTGTCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACACTGGGTATATAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAACACGAGAAATGAGAAAAAGGAGAGGAGCAGAGATTCAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGAACATTTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTATGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACCAACCCTCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC
 CAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTACGGTCTCCTACA
 TTT**TGA**TCCCTTTTAAACCTTACAAGGAGATTTTTTATTATTGGCTGATGGGTAAAGCCAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTGTTTTTACTATGTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCACTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTTCAAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGAAAAGCAAGAATAGCCTTAT
 TTTCAAATATGAAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATTCCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLVDVNDLTLMEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCACAGCCGCGCGCGGAGGCGAGAGTCAGCCGAGCCGAGTCCAGCCGACGACGGACAGCGCAGGGCGAGC
 CCAAGCAGCGCGCAGCGAACGCCGCCGCCGCCACACCCCTCTGCGGTCCCGCGCGGCCCTGCCACCCCTTCCTT
 CTTTCCCCCGGTCCCCGCTCGCCGCGCAGTCAGCTTGGCGGTTTCGCTGCCCGCGAAACCCCGAGGTCACCA
 GCGCCGCGCTCTGCTTCTCCTGGGCGCGCGCGCTCCACGCCCTCCTTCTCCCTTGGCCGCGCGCTGGCAAC
 GGGGACCGTTTGGCTGACGCGAGCGCCAGCTCTACTTTTGGCCCGCGTCTCTCGGCTCTGCGCTCTTCCAC
 CAACTCCAACCTCTCTCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGAGCCCTCGGCCCGCTGCGGTAG
 CGCGCTTCCGCTCCGCTCCCAAAGGTGGGAACGCGTCCGCCCGCGCGCGCACCTGACGCGGTTCGGCTTGGC
 CCGCTTCTCTGACCCCTGGCAGTGCTCAGCGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AAGTGCAGCTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCGCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCGCTCGAAAGTAAAGA
 TGATTTCAAAGTGTGGTTCAGCGAACAGTGCATATTTGCAAGCTGTCTTTGCTTACAGTTACAAGAAGTTTG
 ATGAATCTTCAAAGAACTACTTTGAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTTGGTGAATCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAATTTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGCTGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCGCTGTTGAAGATGATCTACT
 GCTCCCACTCGCGGGGTCTCGTGACTGTGAAGCCATGTACAACTACTGCTCAAACTCATGAGAGGCTGTTTG
 GCCAACCAAGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTTCAACATTTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG
 ATAATAGTGTTCAGTGTCTCAGAAGGTTTCCAGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTT
 TCTCGTTCATCTCTGAAAGTGCCCTCAGTGCTCGCTTCAGACCACTACCCCCAGGAAACGCCAACCCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATTTCTGTCCT
 CCCTTCGAGCAGACGTTTGAACAGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGTGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACTGTTTTCAGTGACAGGAAATGGAATAGCCAACAGGGCAACACCCAGAGGTTCCA
 GGTGACACCAAGCAACACGACATACCTCTCGTCAAACTCATGGCTCTTCGAGTATGACCCAGCAAGATGA
 AGAATGCATACAAATGGGACGACGTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAGAAAGAGTGGAAATG
 GGCTGTGATATCAGCAGTGCCTTTCAGAGTTTGAATACAAATGACCAAGTACCACTGACCATGCTGGGAAAGTGCCTGA
 GAAAGCGCAGTGTGGTGTCCGTCTGGGCAACAGGCTACCTCCTCACTGCTCTGCTGATCTGTTTCTCGT
 TTATCAGAGAGAGTGGAGATTAATCTCAAACCTCGAGAAAGTGTTCATCAAAAGTTAAAGGCAACAGTT
 ATCACTTTTCTACCTCTCTACTGACTTTCCTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGC
 CACTGTTTAAAGATGCTGCTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAGGCACTGTGCATTTGAGTTGGT
 TCCTGCTCCCCCAACCATGTTAAAGTGGCTAACAGTGTAGGTACGAACTATAGTTAGTTGTGATTTGTGA
 TTTTATCACICTATTTATTTGTTGATGTTTTTCTCATTTTCGTTTGGTGGGTTTTTTTTCAACCTGTGATCT
 CGCCTGTTTCTTACAAGCAAAACCGGTCCTTCTGGCACGTAAACATGTACGTATTTCTGAAATATTAAAT
 GCTGTACAGAGCAGGTTTTATTATCATGTTATCTATTAAAGAAAGCCCAAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSLPSNVCNDERMAAGNGNEDDCWNGKGSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILLRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCGA**ATG**AAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAAGC
 AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAACAATGTGAGCTAAGAAGCTT
 TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
 GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
 CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGCTCTC
 TCTAGTGCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCTCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCATTAACTTTAAATGC
 AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQPCDHFPGNVKTRHQRHHRKPNKHSRACQQLKQCCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
 GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
 AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
 GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
 AACATTTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
 GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCTCCAGGACAGAGCCCTCAAAGCAAC
 TCCCAACGAGTTCTCAGGATTGAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
 CTGACTGCATTTTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
 ATGGAGAGGAA

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FIGURE 101

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDDKPDPSGKDPKPDFFPKFLSLGTEIENAVE
FILRSMRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCTGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGCTTGAAGGATCTTGAGAAGCCCCAGTTCTCCGAAATCCAATAGG
 AACGACAGCCCCCTCCCTTGAAGTGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAAC
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC
 CCTTTCTTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCTGAGGCTACACCCATGCGT
 CTCTAGGAACTGGTCAAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCAGGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACACG

FIGURE 103

MDILVPLLQLLVLLLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCCTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFM
WQQVFEPWTKHIGDGCCLTRETWKDLNAQFSEIQMERQPPPLKWLPVGPIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYPLRGT

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FIGURE 104

GTGGGATTTATTTGAGTGAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAG**ATG**TCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCAACATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTCAGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTTGGCTATCTTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACTTGACGGAATGGAACAGCAGAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT
 GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCGCCACCTTGGTTCCAGTGCTGGA AACGATATTACCTCAGTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCCAACAGGCAAATTC AACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAG**TGA**AACAGAATTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTCAGCTAGGTAAGATGACAAACTGCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAAGTATGCTAGTTAGCTAGCTGGTACAGA
 TAATTCAAACCTGCTGTGGTTTTAATTTTGTAACCTGTGGCCTGATCTGTAATAAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTD SGIVGPQFIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNTNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGGCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

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FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGACAGGGAACGCGGGCGGCCAGACAACGGG
 TGGGCTCCGGGGCCTGCGGCGCGGGGCTGAGCTGGCAGGGCGGGTTCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACCCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTCAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCATAACTTTTGAAGGAAAGTAAAGGAGGATCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCACTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTATACTTGAGTTTTTGTGTGCAAC
 CTGACGGAATGAAAACGACAGAATATAACTAACCAACTGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGAAAAACGATATTACCTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTCCA
 GACCCAAACAGGCAAAATCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAAATTTGAAGTGAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAT
 ATGTCCTCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTACAGTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA
 AAAAAA

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FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCT**CATG**GGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACC**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGCCTGGGGTGGGGGCTTATGAGTTGGTGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAA**AACT**GGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCTGGTCTCCAGTGTTTGCTGGATAATA**AAAT**GGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLP TLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPSLEPRT

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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCATAGTGGA
 TCA**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTTAGCCTTGTCTTTGGCC
 ATGATGTTTTACCTTCAGATTTCATCACCACCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGTCTGCTCGTCTTGATTTTTTGTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCAAATCACAAATAAGCCATCAGCAGTGTCCCTTCTGCTGTGTCC
 AGCCACTGTGGACATTTGCCATCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCAAGTGGAATATAAGCCCT
 TTCGGGCATTCCGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAATCATTTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCATTTTCTGTGTTTGGCTGTTGAT
 CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCTATTCTTCTCTCAAA

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FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNPPDHPILSSLSILFFYHQGTVVKGSEFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAAATATTCAATCTGT
 TGTGGTGAATAATTTTTGAAAAAAAATTTGCCTTCTTCAAACAAGGGTGTCATCTGTATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTCTTGTTTGTCTGG
 TGACTGGAGTACATTCAAACAAGAAACGGCAAGAAGATTAAAAGGCCAAAGTTCACTGTG
 CCTCAGATCAACTGGGATGCTCAAAGCCGGAAAGATCATCGATCTCTGAGTTCATTGTGGAATG
 TCCAGCAGGATGCCAAGACCCCAAATACCATGTTTATGGCACTGAGTGTATGTCATCTCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGGAGGAAAAATCACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCACACGGTGTCGAATCGTT
 ATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAA
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAGCCCTATCAGAGGCCACCTATTCCAGGGACAACATGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACACCTTGCCAAAGGCCATCCCCCTTCG
 CTGCTTCTACCAACAGCATCCCCAGACCACAAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCAAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGCGGATCTCAGCCCTGGGAC
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTCTGTTTAAATTGATGGGAGCACCAGCATTTGCCAAACGGCGATTCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTTTGACATTTGGCCCTGCCCGTCCAC
 TGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTTCACTTTAACTTCAAGACACACAGC
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCCGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCCAAAGCCAAATGGAAACAGAGGCG
 GGGCTCCAAATGTGTTGGTGGTGATGGTGGATGGCTGGCCACGGCAAAAGTGGAGAGGCT
 TCAAGACTTGGCAGAGAGTCAGGAATCAACATTTTCTTCATCAACATTGAAGTGTCTGCTGA
 AAATGAGAAGCAGTATGTGTGGAGGCCAACTTTGCAAAACAAGGCCGTGTGCAGAACAAAGC
 GCTTCTACTCGCTCCAGCTGCAGAGCTGGTGTGGCCCTCCACAAGACCTTCAGGCTCTGGTG
 AAGCGGGTCTCGCACTACGCCCTGGCTGCGACGAAGCTGCTTGAATCGGCTGACAT
 TGGCTTCGTCTACAGCGGTCCAGCAGTGTGGGACGGGCAACTTCCGACCGTCTCCAGT
 TTGTGACCAACCTCACCAAAGAGTTTGAGATTTCCGACACGGACAGCGCATCGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCGACAAGTACAGCAGCAACGCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTCGCCTCGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGGAGGTCCTACGACGAGCTCCGGATCCAGCCATGGCTGCCATCTGAAGGG
 AGTGATACCTTATCGGATAGGCGTTGCCTGGGCTGCCAAAGAGGAGCTAGAAGTCATTGGCA
 CTCACCCGCGCAGAGACCCTCCTTCTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC
 CCGAGGATCATCCAGAACAATTTGTACAGAGTTCAACTCACAGCTCGGAAC**TGA**TTACAGAG
 CAGGCAGAGCACAGCAAGTGTGCTTTACTAACTGACGTGTTGGAACACCCACCGCTTAA
 TGGGGCAGCGCAGGTGCATCAAGTCTTTGGGCAGGGCATGGAGAAACAAATGTCTGTTATTA
 TTCTTTGCCATCATGCTTTTTCATATTCCAAACCTTGGAGTTACAAAGATGATCAAAACGT
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTACATTTGACAATTT
 GTTTTCAAATTAATGTTCGGAATACAGTGAGCCCTTACGAGGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTCATTTTT
 GTCATGACATGTAGGAATTTGCTGAATTAATGTTTGAAGAGATGAATAATTAATAATAATA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKLTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI PAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI IQNICTEFNSQPRN

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FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
 TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGCTGGAAGTAGA
 GGTGGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACTCC
 TCCAGCCTTTTCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAATACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCCTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGAGGAAGCGAGAGGGGTACCCA
 CTTGCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATGCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGTGGGGGTACAA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTAGTTGCGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCTATAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

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FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPGTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYTIVWKQFG
GLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRATGDPPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

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FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCAATCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGAAAGAAACAATGTCTAGGTCAAATGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGTCTACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGTCACCTGTTCTGTCTGGAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCCGAGACCTTGAAAATAACCAATTCACCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGCGCTGGAT
 CTCAT**TAG**GTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 GTTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAA

FIGURE 117

MQFTTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS
SILKHPFNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFMILIV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

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FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTACAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAAC TGAGTCTACCAAATGCAGACTTTCACAATGGTTC TAGAAGAAATCTGGACAAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGT CAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTG TGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGG
GTTNGCGAACCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**TGGCGGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGTGCGGCCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGGAAACTGGTGTGCTGAGAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGGCGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGCCAAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
 TGGTAGGGGCTTGGGACCCAACCTGTGTGAGTGGAGGAGGTGAGCCCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTT**TAA**CCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
 AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCACGATATAAAAAATAAAATGAAAGTATCCTCCTCAAAAA

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHFAFKYLAQTSGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACCGGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATGG**CTGTCTACGTCGGGATGC
 TGCCTTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCGGGCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTACGGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCTGGAGACCACAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTCGTCCTCCATGAAGACGTGAGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCTTGTGTTCCTCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAAATGCCAGCCAGGGGGCTTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCGGGGACCCTGCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCTCTGTCTGCCATG
 ACCCATCAACATCCAGTTTCACTCTCGGGGACAACAGGCAGCCCCAGGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCAACCCTCTGTACCATTGCTTGGGTTCCGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATTGTGGAG
 GTGTCAATGCTGGGTCCCTGCCACCTCCAGAGTTGATCCGAGCCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAAGCTCCCGTGACATTGCGGCACCT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCTTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGACGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGATGGGGGAAGAGATTGTGCCTGCATTGCGCTGAAGGACCGGGGAGGAGACCACGG
 TGAGGAGATAAAAAGCTTCTGCAAAAGGAAGATCTCTCACATTCAGAGTTCGGAAGTACATC
 GTGTTTGTACAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATCAAACTTCGAGA
 GCAGATGGAACGCATCTAAATCTGT**GA**ATAAAGCAGCAGGCGCTGCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCACCCAGTTC
 TGAGCCAGGCACATCAATGTCAAGGAATTGACTGAACGAATAAGAGCTCCTGGATGGGTC
 CGGGAAGTGCCTGGGCACAAGGTGCCAAAAGGCAGGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCTCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

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FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVDMMVSTPIGGLSYVQ
 GCTFKHLNSKTGVQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDVVAAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPTVFAHFPEDTVEQKAESVG
 RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGGENIYPAELEDFHHTPKVQEVQVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTCCTGGGTTCGGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCAGCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCCATGGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCCGCGGTCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACCTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGGCTCCCGGATGAGGAGGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTCTGTTCCCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGCGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTT
VASTTSVTTSTSApVRPTSTTKPMPAPTSQTPrQGVeHEASrDEEPRLTGGAAGHQDRSNG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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[illegible]

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCC**ATG**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCCTGAACCTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAG**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

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10021-226860

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

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FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTT
TTCTCCAGCCAGTTCCAATCAGGAGACAGGTCCCAAGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTGTTTATC
TTCACATATTAATTGTAACGATTAAAAAAGAATAAGAGCAGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGCGC**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTATTGACCAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATCTCTTCTGTCTCGGAAAAACCCAAACTTGTGTTATGCAGAATACACCAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAAATTAT
 TCCCAAAATGTTGAAAACCTGAAGT**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD A EYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYL FNFRGVAASFRFKHLFLCGSLVFHVGD E WLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSY
NVTRRKG YDQIIPKMLKTEL

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FIGURE 134

CACCCCTCCATTTCTCGCC**ATG**CCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCAGTACTTTGGGGTCCCTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTGCACTGGTGATGCCGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCACGTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATCTGAGTTTCAGCCA
 CTGAACCTCAAAGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACCTCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCTCCA
 GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLIPAAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVVP TLTGDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

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100211.326660

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAAACAACAAAACTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCGGGTTGACCTGTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTACCCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGCATGCGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCAGTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGCTCACTCCTGAGTTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATGTCTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAACGTAGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
 TGTTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAACCCATCAAGTTT
 GAAGATGTTTATGCTGGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTAAATAAAGTAGGTACTGTGAAAAATTATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAAATAGGACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAACAAAAACAATGTAGAGTTTTATTATTG
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTTATCTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAAATGTAAAGTCATAGGTCAATTATTGCATATCAGTAATCTCTTGGACTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAACTGAAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNL LKVNIHIPEDTNLFFLYRIHL DVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCCTAGCTAACTATAATATCAACGTCATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

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FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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CATTCTGAAACTAACTCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCCGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAACCTCAGCCCTTTCAACCTCGGTGGATTTTCTCCAGCCTCCAAGCC
ATCATCCACCAAGAGAAGTAAAAAGCTGAAGAGAAATCACCATTCTCCATTAAATGTGAAGACAG
TCAAAAAGACAACCTGAGGATAGACAAAGGCTTCCAAAGCCCTTACAATGGTGTAGAAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAGATGCAGGTCAGAAGACAGCATCAGC
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCGCCGAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCTATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGCGAGGCACAGGCG
CTCACTTTCTCTTCTTTGAGCCTGCATAGTTCCTTGTTTTGCTTATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAACAGCAAACCTGATTAGGATTTGATTTCTTGAACCCCTCA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTTATTGCTATAAGAAGTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT
ATACAGTATAAAATTCGAGACACTGCTCTATTAAAGTGGTTATTTGTTTAAATGATGGTGAAT
ACCTTCTTAAACACTGTTTTGTCTGCATGTGTAAGATTTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTTCTAAAAAAGAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSTRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKRSRSQ
SKSRDHSDAAKKHRHERGHRDRRERSRSFERSHKS KHHGGSRSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTtagagtaatttctagtttggattgtaatatgaaattattttaaaagggttcgct
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAAATAAGAGAAGAAAAAAGA
ATAAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAAGCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

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FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGT**CATGGC**
 GGTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCGTTCTTCTCGGAGTACCACTGG
 TTTGTGGACTTTGTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGAAGTGGTGGC
 GGAGGAGACCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGCTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGAGCGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACCACTTCTCTGTCTCCCTGTTTCATCTGTGGCTCTGGACAAAGCCCATTGACACGGGAC
 TTCTTGACACAGCCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCATACCTGTGCTTGGCCAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCACTACCTGACGCGCTCATCTCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
 GGCTC**CTAG**CTGCCTGCAGACCTCCTGGGGCCCTGAGGTCTGTTCTTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCCCCCGTGTCCCGAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGGTTCCCTTACACACAGTGCCTGACCCGCGGCCCCCTTGGACGCCAGTTTCTGCTCAG
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCAGGGCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

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FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTIVTRLYFSAEEGGERSVCLTFAPFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWOWALPVAKLAIKRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSQYLTPLILTLCNTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAAARI
AGALGGLLTPLFLRGVLAyliWWTAAcQLLASLFGlyFHQHLAgs

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FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

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FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAAAGTGGCTT
 AATCTGAAGGTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCAGGGAGAATGCAGCACATGCTCGGAGAAATGAAGG
 CGCTTCTGTGTGCTGTCTTGGCTTGGCTCAGTCTCTGCTAACTACATTGACAAATGTGGGCAACCTGCACTTCTCTG
 TATTCAAGACTCTGTAAAGGTGCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGGAGCCTCAGAGCCACGGCTCCCTCCCGAGAGGTTTCTGAGCTGCCACCCTCTCCTTAA
 TGACAGACGAGCCTGGCCTAGACAACCTTGCTCTGCTCGCCAGAGGACGGGCAAGCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCAGGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAA
 AAAATAAATCAGGCTTTGAGTGTTCTCGAAGGACAAAGAGCGGGAGTGCACTTGCCAACCATGCCGACCAGG
 GCAGGGAAAATCTGAAAACCACTGCCCTGAAGTCTTCCAGGTTGTACCACCTGATTCCAGATGTTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAAGTGAAGCCCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACACGCTGTGCGTCTCTCGCG
 CAGCCCTGCCAGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCCGCAGCAGGAACAATGGACAGGCCCC
 GGATGCCCTACAGACCCCGAGATGACAGCTTTCAATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTCTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCAGCCAGAAAG
 TGGCGCTCATCTGATTGAGGCCAGTGAAGACGTGTTCACTCGTGTGCCGCCAGGTTCCGGCAGCGGAGCC
 CTGACATCTTTAGGAAGCCGGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACT
 CCCCAGCCCCCTCCATCCTACAATTACTTGTATGAGAAGGTGGTAAATATCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGACGGGGAGCATCACATAGAGAATGGGATTTGGCTATCTATGTATCAGTGTTAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACCTGACA
 GAGGTGAGCCGGAGTGAGGAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGATGACAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCACGGTGCTGTATAACTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTATGAGAATAACATGGAACAAACCTTT
 TTTCTCAAAATCCATTGTTGAAGGAACACAGCATCAATGATGGAAGAAATAGATGTGGTGATTTCTTCTGT
 CTGTCAATGGTGAAGTACATCAGGAATGATACATGCTTGTGTCAGACTGCTGAPAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTGGGCTGGCACTTTTTTATAGAAATCAATGATGGGTGAGGAGAAACAGAAAA
 TCACAAATAGGCTTAAGAAGTTGAACACTATATTTATCTTGTCACCTTTTATATTAAAGAAAGAAATACATTGT
 AAAAATGTGAGGAAAAGTATGATCATCTAATGAAGCCAGTTACACCTCAGAAAAATGATTCCAAAAAATTA
 AACACTAGTGTTTTTTCTAGTGTGGAGGATTTCTATTACTACACACATGTTTATTTTTTTCTATTCAAT
 AAAAGCCCTAAACACTAAATGATTGATTGTTATACCCCACTGAATTCAGCTGATTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCCAGGGTACATTTATGGCCATTTTAAATTCAGCTAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTTCACTCAACACAGAATAAATATTTTCAGAAGTTAA

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FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKVDPEGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISR DGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

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CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCTCTCCAGGCA**AATG**GTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACTCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAATCATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGACTATAAACATGGGTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCCGGTGTGGAGGCTGTGCAAAGGCTGGGCTCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATCATGCTTT**TAGG**ATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACATCAAAGTCAAATTAATTTCTTTCCCAATGCCCACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATATA

FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNI PPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTAGGAGGTTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCACAAAGTCCTGGAAGTTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCTT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCCAGGTGGTGACAGAAGATGGAGGACTGCGAGGTCCTTGGAGA
 GCCCATCTCTTGCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGAGGTGAGAGGACGCAAGCAGCAGCCATG**TAGA**ATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCCTGTTCTGTTTGGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPFITNSLIGKDQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESFILALPLYRSTRRLSEEEFG
GFRIGNGEVGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FIGURE 152

GGTCCTTA**ATG**GCGAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCGTGGGGAAGAAA
 CTAAATGTCACAACGGCTTGGAAAGCACAGAACCCTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTACAGTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGCTGCCCTCCTCATCCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACAAAAGGCTCCTGTGAGCAGG
 GTCTTGATCAAACCTGCGCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCAGTGCCTTGATTCCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTAC
 TGATGGAATTCCTGCACCTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTGTTGAAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAAAATAACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTTAAATATTATTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAATKILLCLPLLLLLSGWSRAGRAPHSLCYDITVIPKFRGPRWCVAQGGVDEKFTL
HYDCGKNTVTPVSPLGKKNVTAWKAQNVLREVVLDLTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQSFDFGQIFLLFDSEKRMWTVHPGARKMKEKWENDKVVAMS FHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTTCGAAAACCCATCTATACAAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTTTCATTCTGTTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCCTGTAT
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRRLKLGQPTEQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAG
 CTCTTTGTTGGCAGGTAACGTGTGCACCACCACACCTGGAAATGCCATCCTGCTCCCGTTCTGCTA
 CCTCACGGCCCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGGCTCGTGCAGTAACCAAGTTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCTGCAGT
 TGGGCAGGAATCCATCCGGCAGATTGAGGTGGGGCCCTTCAACGCCCTGGCCAGCCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAAGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAACT
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCACTGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACAGGCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAATCTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACTTTTCCACGTGCTGC
 TTTTCAGACACTGGGGTGATACATGTCATGGTGACCAATGTTGAGGCAACTCCAAGCCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCCGAAAGTACAAGCCTGTTCCCTA
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCCTGACAAGATGCAGACCAGCCT
 GGATGAAGTCAATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACACGACGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCCG
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGGCAGTAGTGCTGCCCAAACTT
 ATGACCATATTAACTACAACACCTACAAACGAGCACATGGGGCCCACTGGACAGAAAAACAGC
 CTGGGGAAGTCTCTGCACCCACAGTCACCACATCTCTGAACCTTATATAATTTCAGACCCA
 TACCAAGGACAAGGTACAGGAACTCAAAATTGACTCCCCCTCCCCAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
 TATGCTTATATATTAAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAAAAATTTAAAGA
 CAAAAAGTCAAAACA

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FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYLNLGMCNIKDMPNLTPLVGLEELEMSEGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSSLPHDLFTPLRYLVELHLHHNPWNCDILW
LAWWLREYIPTNSTCCGRCHAPMHRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSSVKWLPLNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAEINTSNYSFFTIVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQORS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPITIHHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQHTKDKVQETQI

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FIGURE 158

CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCC
 TTCTCATCTCGTCCCTTGCCAGAGAGTACACAGTTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG
 TGTGGGAGTGTGTGAATATGATCAGATTGAGTGCCTGTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCAT
 CCCTTGCTGCAGGAATAGGAGAAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAACAT
 GCAAGAGCTCGCGAAATGGCTCATGGGGGGTACTTGGATGACTTCTATGTAGAGGGTTCTACTGTGCAGAG
 TGCCGAGCAGGCTGTCAGGAGGAGAGTCGATGCGATGTGGCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTT
 GTTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTTCATGCTAAACCTTGGGTTTGTCACTCAACATTA
 GATTGTGTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGCAAC
 CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT
 CCACGTCCTCTTCCACTCCGATGGCTCCAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT
 GCTCCTCATCCCCTTGTTTCATGACGGCAGCTGCGTCTTGCACAAAGGCTGGATCTTACAAGTGTGCTGCTTG
 GCAGGCTATACTGGGCAGCGCTGTGAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGCCAGTCAA
 TGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGAGCCCATGCTAAAATTTGCCACCCTGGTGTCTT
 TCTTTTGTAAACACTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTGCCAGCAGAATGGAGAGTGGTCAGGG
 AAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATTTAGACCTGGTGAGAAGGAGAGTCTTCCGAT
 GCAGGTTTCACTCAAGGGAGACACCATTTACACAGCTATACTCAGCGGCCCTTCAGCAAGCAGAACTGCAGAGTG
 CCCCACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCTTCTACCGCGCCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG
 TGGGCGGGCACCATCCTGCATCCTATCTCGGGGAAAATGAGAACATCACTGCTCCAAAGACCCAAAGGGTTGC
 GCTGGCCGTGGCAGGAGCCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCCTACACAGGGAGCGTGG
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTACTGACCTGGG
 GAAGGTACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGAAATTTACCGGGATGATGACCGGGATG
 AGAAGACCATCCAGAGCCTACAGATTCTGCTATCATCTGCATCCCAACTATGACCCCATCTGCTGTATGCT
 GACATCGCCATCTGAAGCTCTTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAG
 TCGGATCTCAGCACTTCTTCCAGAGTCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGCGTGAGGA
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCACTGTGGTGGACTCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGAAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCATGCCCCCTC
 TGATATCTGCATCGCAGAGCAGGAGGCATCGCGCTGTGTCTTCCCGGGACGAGCATCTCCTGAGCCACGCT
 GGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAACATGCAAGCCACAGGCTCTCCACTGCCCTTCAACAG
 GTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTTC
 TGTATATCCGCTCTGTACTGTGTCAATTGCGTGAAGCAGTGTGGCCCTGAAGTGTGATTGGCCCTGTGAACATGG
 CTGTGCCAGGGCTTCTGACTTCAGGGACAAACTCACTGAAGGTGAGTAGACCTCCATTGCTGCTGTAGGCTGAT
 GCCGCTCCACTACTAGACAGCAATTTGGAAGATGCCAGGGCTTGCAGAAGTAAAGTTTCTTCAAGAAGAGACC
 ATATACAAACACTCTCCACTGCCATGACCTGGTGGTCTTCCCAACTTTCAGTTATACAGATGCCATCACTTG
 ACCAGGAGAGTCTGGGCTTCATGAGGGCCCTTTGAGGCTCTCAAGTCTCAGAGACTGCTGTGGGACAGCC
 CGGCGCAGAGCTGGGATGTGGTGCATGCCCTTGTGTACATGGCCACAGTACAGTCTGGTCCCTTTTCTCTCC
 CCATCTCTTGTACACATTTTAAATAAAGGTTGGCTTCTGAACACAAAAAAGGAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA

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FIGURE 159

MELGCWTLQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIPCCRNEENECDSLHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHGD
TCVLDKAGSYKCACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPH
QLYSAAFQKQLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFYRRGLSSRRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSVHDSGLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPPFKDWIERNMK

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FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGAAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGGC
 TTCAACCTGACTTTCCACCTTTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCACTAACTACTTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGTCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCGGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCAGAGTGGAATTTCTGGTTTGGTGCAATGACCCCTGGATCTTTTGGTGATGTTTGG
 AAGAACTGATCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTGTGAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTCAAGTGAAGAAGCGCTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGTGGAGTGTCTGGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAATA
 TGTCTATCAAAATACCTCTGTAGTAAAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKÇEEHPKHLVVG RNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTGCGCAGCGGGCTGTGGGCGCGCCGGAGGAGCGACCGCGCAGTCTCT
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCA**ATG**
 GCCCAGGCAGTGTGGTGCAGCTCCGCGCATCTCTGGCTTGCCTTGCCTTCCCTGCCCTGGGC
 CCCGGCAGGGGTGGCCGAGGCCCTGTATGAACCTCAATCTCACCACCGATAGCCCTGACCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCCCACTTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTGGGCCACGTCGCCGGGGAATTCCCGG
 TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTTCCCCATCACAGAGTTCCTCGTGGGGACCTTGTGTCAACCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTCACATAAGACCGTCCCTGAAAGTCTCCTTCTCCTCCACGACCCGA
 GCAACTTCCCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCCGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCGCCTCCGTGAAAGCTGCAGGAAACCCCTCGAGGCATCCAAGTGTTTGGG
 CCCACCCCTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCCTCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGCTGGCCAGCACACGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
 TGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTGGCTTCCCATGTGCTACACTTATCACTGTGA
 TGTGGGCTTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAAGGACATGGTGGAG
 AACCCGGAGCCACCCCTCTGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTTGCT
 GGAGACTCCATCTGAGTACCTGGAATTTGTTGCTGAGAAACCACGGGCTGTCTCCGCCCCCTCT
 ATAAGTCTGTCAAACCTTACACCGT**GTGA**GCACTCCCCCTCCCCACCCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAAT
 TGGCTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTTCAGCCACTGCCACAAGCC
 CCTCCCCTCTGTGTCACCCCTGACCCACGCCATTACCCATCTGTAGACTCCAGCCACTGACA
 TAAGCCCACTCGGTTACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAAGGACTGAC
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCCATGCCATTCCT
 CTCATATTGGCACATCTGCTGCCATTGGGGGTCTCAGTTTCCCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGATGACACACACACACACACACACACAC
 CACACACACACAGAAATATAAACACATGCGTACATGGGCATTTCAAAGATGATCAGCTCTGTA
 TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACAGCTAGAGCTGAAGGAAATTTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAAGTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCCCTGGATGGGGGGCAGGACT
 AATACTGAGTGATTGCAAGTGTCTTATAAATACACCTTATTTTACGTAACCAACCATCTGTG
 AAACCTTCACTGAGGAAAGGCCTTGACAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG
 TGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCACCTGGTATAACAGCGGTGAACCCCGTCTCTACTAAAAAATAACAAAGTT
 AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGACGAGGAATG
 GTGCGAACCCGGGAGGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCATCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSIRAENIIISKTHQYHKIQVWPSRIQPAVFAFPFCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCOMCCGFLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCTTTTGTTCCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

00000000.11111111

165/330

FIGURE 165

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQFQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

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FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACCATGTTCTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCTCTTACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTTCAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTCTGGAACCTGCTGAGCAGAACCAATTATACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGTCTGATTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAACAGACCAAGAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCAGTCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGTGAAGGCCGT
 CCCACAGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAGCAAGCTGCCTATCTCATCTTCCAGGAAGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTATCCC
 TGTGTCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGACAGCTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
 AAGGACAGGAGCCGCTCTGAGCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACCTGCTGTCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCCGCCAGCCGACGCGGGATCCGCTG
 GCACCCGGCGCAGCCTACCCCTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GCGCGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCCG
 CTCTCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCTATCTGCAGGGGCTTTTACGAAAAATG
 AAGGGTATGATTTTTATGCTGCTGCTGATGGGGTACTAAAGGAGGGGAAGAGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGACTCCAGGCTAACCCCTGAATCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGCTGGTGAATCTTACCTCACAGGGCTGTTGTGGGGATTAAAGTGTGCTGCGGGTGAAGTGA
 AGGACACATCAGTTTCACTGTTTCAAGTACAGGCCACAAAACGGGGCAGGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAAEELSWNLLSRTNYNFYISLRRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGACCCCTGGCCCTCA
CGTCTCCTCCAGGG**ATG**CGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACTATGTGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGGCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTA

CTGTAAGGCGCTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCAATCTGAGGGGGCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCC**TGA**AAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGCTATGTGATGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
 TATTGTCTGGACCTTCAACACAAACCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGTCTCCTGTTGGTGGCCCT
 CCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCAT
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACATAATAGAACAAATCCTAAAGGAAGA
 TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
 TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
 CACTCCCCTAAGTCTCTGCTCA

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FIGURE 171

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEVDIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTAAAGAGCTGGTTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTTCGGGAA
ACTCCTAACATATGCCCCCATCTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
AGATGGAAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAA**ATG**AAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAGACTTCTTTAAATTTCTTTTGATACACCTTGACAAT
TTTTCATGAAATTATTCCTCTTCTGTTCATAAATGATTACCCTTGCACCTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
 TGGATTACGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
 TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCATCTCTTGCTTTGAGTGGTGGTTC
 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
 AAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA
 CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCTCTC
 ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
 CATTCATCCAGAATCCTTCAACTGTCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
 GTTTCATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
 TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTLAGGTCTATTGCT
 TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCTTGGCTGTC
 TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
 TCAGTAGTTTGAAAAAAAAA

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FIGURE 176

MTCCGWTSCNGFSLVLVLLLVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGCTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAACTTAATCCACCTCCAGAAGCTCTTGCAAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCGATCCTGGCTTGGACCTATGCCTTCTATAACAAGCTGCCGCCGGCTCC
 AGTGTTTCCACAGCCCCCAAACGGAACCTGGTTTTGGGGTACCTGGGCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCAAGGATAATCTCTTCATCAGGTTCTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCGCCACCCTCGGATGCTGAC
 GCCCGCCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGAGGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCAGATGGACTTTCTGTATTACCTCTCCCATGACGGCGGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTATCCGGGAGCGGCGTCG
 CACCTTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCCAGAACTGCATCGGGCAGGCGTTGCCATGGCGAGATGAAAGTGGTCTCGG
 CGTTGATGCTGCTGCACTTCCGGTTCTTGCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
 GTGACTTTCTGACCATCCACCTGTTTTTTGCAGATTGTCATGAATAAACGGTGTGTCAA

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FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGWSLLARILAWTYAFYNNCRRLQCFQPQPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDFFKDKAKSKTLDFIDVLLLSKDEDEG
KALSDEDIKAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFTSRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCCAAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

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FIGURE 186

MPSPGTVCSSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCGATAGTTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAAGAGTGTCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAAGGTGAGCCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGTGTAACGACGAGGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCCACCAAGA
 GCCTCCTTGTTTCATAACACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIGMLVLLDGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCCTCTGTCCTGTCAAGTCTCCTGGGGATGGTGCCCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCAACCACCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCA**TAG**TAAGAGCTTCAAGGAAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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FIGURE 190

MAKMELSKAFSGQRTLLSAILSMSLSFSSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNSTQEVVQYNWETGDDRF5FR5FR5GMMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPGCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLP5DCQLG5RRLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQH5VHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTGAGCTTTGGCCCAG**ATG**TGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTATCTGTCTCATCTCCCTCACTTAAGTCTCAGGCCGTGCA
 GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCTTCCCCCTGCCCGCCGTAGATTCAG
 GACATTCGCCCTGTGTGCCACCAACCAGGACTTCCCTTGGCTTGGCATCCCTGGCTCT
 CTCTGTTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
 GGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGAAAGATCATCTGCTGCAGATGC
 TGTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAATCTTTATTACTTTGGG
 AAGTCACTCAGCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
 AACCAGGAAACTAACAATGTAGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAAATCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCCTCGGGTCTGGAGGCCAGGAGCGACGTCA
 CGCCG**ATG**GAGCGATCAAAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGAAGTGATGTTTTTGATGCTT
 GGATGTGCCCTTCCAATATACACAAATACTGGCCCTCTTTGTTCTATTTTTTACATCCTTTCCACCTATTCC
 ATACTGGCATACGAAAGAGATTAGTGGATGATACAGATGCTATGATTAACGCTTGTAAGCACTTGGCATCTTTC
 TTACAGCGGGCATTGTCGTGTCAGCTTTTGGACTCCCTATTGATTATGGCCAGAGCACATCTGATTGAGTGGGGA
 GCTTTGSCACTTGTCTCAGAGGAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGGA
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTAAGTAATTTGTCAATGGACTTCCTGTCATTT
 GTTGGCCATTACGACACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGTGAAGGATTAAGAGGATTTTCT
 CTTTGGAAAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTCTGTAGGTTGATTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATT
 TAGCCTCCATTATTACAAAAAATATAAAAAAAGTTTTAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTAGTGCAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTGTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAAGAATTTATGTTAACTTTA
 AGGTAAGGGTGTA AAAACATTTTGAGATAAGGTTTTTATTATGTTTATATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTTCATGTTTTTACCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTGTGATGTTGTC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCCCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAAAATATAGTTTAAATAACACTTGAAGTGTTTACTTACCTGAAAAAATTAATGCTATGCCGTACATT
 CAGAGTGCCCTCCCTGCAAGCCCTTGCATGATTAAACAAGTAACTTGTAGTCTTACAGATAATTTCATGCA
 TTAACAGTTTTAAGATTTAGACCATGGTAAATAGTAGTTCTTATTCTCTAAGGTATATATCATATGTAATTTAAAG
 TTTTCTTAAGACAGTTTCTCTGATACCTCTGAAGCTGTTTGTATTTGAGTCTGAGTATAGATGCTGCTGTT
 CCTTATAAAGGCAATTTGTTGTGAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAATTTCCGATTAACCAAGGCTGATCAATTTATAGTGTGCTTTACATCTAATAAATATCAGGA
 CTTTATTCAGGAGTGGGTTATAAAAAACATTAAGTTGGTCTGACAGTATTTTGTAAAGATATTTGTTGTATG
 TTTATGAGTTTATTTCTCAAGAAAAATGGGAATAAATTTGGGATTTGTTAGCTTTTTTACTAAGATGGCTAA
 AGCCACAGGTTTTATTGCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAATATCG
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTTGATTAATAAGTTTCAGATTTCAAGAGGAA
 GGTGCAAGTACACATGAGTTAGAGAGCTGGTGAAGAGTTGGGAAGCTTTTGTGCTGTGATCTACTGGACTTT
 TTTTTGCAAGGAAGTGCAATCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAGTGCCTGCTACTG
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTCGATTTGGCAGCAT
 GTGCTTTGACCTTTGATACTAGCTTGACATAGTGCTGCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATATGACTGATACAACATTACCATTCTCTATGGAAAGAAAGCTTTTGATGATGAACAAATAA
 AGATTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFSGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAGFLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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FIGURE 195

CCCACGGGTCCGCCACGCGTTCGCCCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC
 CACGGCTCCGGTCCAGCTCCGCCGCCACATGCTGGTGGAGGGAAGGAGCCGGGGCGCTCTCCGCCGCTCC
 CGCGCCGCCGCTCCGCACTCCGACCGCCGCCGCCGCCGCCGCCGCGGCAAGAGCATGAGTGAAGCCGCTC
 TCTGCAGCTCCGCCGGGGCGGAATGGCAGGCTGTTTCGCCGGAGTAAAGAGGTGGCGCGGTCAGTGGTGGTTT
 CAATGACGGACATTAAACCGACTGTCAGATCTCGGGAGTCGCGAGCCCGAGTTTGGAGTTTTCGCCCCAC
 AACCTCACCTCCGACTCCAGAGGGAAGAGGCGCGGAGGACGCTCGAGCTCGGCCGCTGATGTTG
 GAAACTTGGGGTCTAGAAAGTCCGCTCCGCCGCTTCCGCCGCCCTTCGACGCCCGAGCCAGGACCAAAAT
 GAGACATTGTGGCCTCGCCAGATTCGCCGCCGCCGCCGAGGCGTGCCTCGGAAACAGAGGGGTCTTCTCTC
 GCCCTGCATATAATTAGCTGCACACAAGGGGAGCAGCTGAATGGAGGTGTGACTCTCTGGAAAGGATTCT
 GACCGAGCGTCCCAATTGGACATTCTCCAGTCTCTCTGGAAAGATTCTCGCTAATGATTTCCTGCTGCTCGGT
 TCTGTCTATCTGGCTGCTGAGGAGGCCCTCGGGGGTGGTCTTGTGTCTGCTGGGGGCGCTGCTTTCAGATGCT
 GCCCGCGCCGCCACGCGGCTCCGCTGAGCTGTGCTCGGTCGAGGGCGCGCTGCTACTGCGAGCTGCTAACCC
 TCACCGAGCGCCCCACAAAGCTTCGCGGCTCTCGGGCTTTCCTCGGCTGACACGCCCTCGAGGCTCGCG
 CGCGGCCAGTTTACCGGGTTAATCGAGCTCAGTGGCTTATCTGGATCACAATCACATCTGTCTCGTCGCGAGG
 GGACGCCCTTTCAGAAACTCGCGCGAGTTAAGGAATCAGCTGAGTTCACACCATCACCAATCGGCCAAC
 CCACCTTCCGGCCCATGCGCCAACTGCGCAGCGTGGACCTCTCGTACAAACAAGCTGCAGGCGCTCGCGCCGCGAC
 CTCTTCCACGGGCTCGGAAGCTCCACAGCTGCATATGCGGGCCACGCGCATCCAGTTTGTGCCCTGGGCAT
 CTTTCAGGACTCGCCGACCTCAAGTTTCTCGACTCGATACAATCAGCTCAGAGATTCAGCGCGCACTCTT
 TCGCGCGCTGTTTAAAGCTCAGGAGCTGCACCTCGAGCACAAAGCACTTGTCAAGTGAATTCGCCCACTTC
 CGCGGCTCATCTCCCTGCATCGCTTGCCTCGGAGGAACAAGGTGGCCATTGTGGTCACTCGCTGGACTG
 GGTGTTGAACTCGGAGAAATGCACTTGTGCGGCCACAGAGATCGAGTACATGGAGCCCATGTGTGTTGAGACCG
 TCGCGCACTGCACTCCCTGCAGCTGGAATCCAAACCGCTCACCTACATCGAGCGCCGGATCTCAACTCTTTG
 AAGTCCCTGACAGACTCACTCCCTGGCGGGAACCTGTGGGATTCGCGGCCCAACGTGTGTCGCTAGCTCGT
 GCTCAGCAACTCTCCGGGGCTTACGATGGCACTTGCAGTCCGCAAGCCGAGTTCGACAGGCGCAAGCG
 TCTTGGACCGCGTGTACGCTTCCACCTGTGCGAGGATGGGCGAGGCCACACGCGGCACCTGCTCTCGGCC
 GTCCACCAACGCGAGTGTCTGGGGGCCCTGCCAGCTCGGGCCACACGCTCGCGGACGCGGGGAGGGGACGCA
 CGAGCGGCATTTCAGGCTGCCAGCTGGCTCTTCCAGGCGCGGAGCACGCGCGAGAGCGGCTGCGAGTCCACA
 AGGTGTTACGGGCAACCATGGCCCTCATCTCTCTCTCTCATCGTGGTCTGTGTTGCTCTACGTGTCTCGGAAG
 TCTTTCACGAGCTCCGCGAGCTTCAGAGTGTCTTTCAGCGAGCGAGGACGAGAAAGCAGAAACAGAC
 CATGTCATCAGATGCTGCCATGCTTCCGCCGAATACGCTGTTTATACAAACCGAACCATTTGAGGAGGCC
 TGGTCACTATCAACGAGTATGCTGTGCTGTGATACCTGCCACAGCAGCGCCGAGGGAATGCGAGTGTGATTGTT
 CAGTGGCTCTCAACCCATGGCTTACCAATACGCTTGGGCAAGCGGGGACGGCGCGGACCAGGCTGGGT
 CTCCTCTGTCTGTGCTCTGATATGCTCCTTGTACTGAACTTTAAGGGGATCTCTCCAGAGACTTGACATTTTATG
 TTTATTGTGCTCTAAACCAAAAGCGAATTAAACACAAACAAACCCACCCACAACTTCAGGACAGCTC
 TATCTTAATTGCTTACGAGAACTCTCTCTCTCTTGAAGATCTGTGCATATTCAGATCTCAGAGATCTCAGAGTAA
 AAAGTGGCCATAAGCAGAGAGAGAAATATCTGTGCTTCTTTATCTACTCTCCCACTCCCAATGATTA
 AACATCATGTCTTGAAGATCTTAAGTCCATACGCAATTTCATGAAGAACCATTTGGAAGAGGAATCTGCAAT
 TGGGAGCTTAAGAGCAAAATGATGACCATAGAAAGCTATGTTCTTACTTTGTGTGTGTCTGTATGTTTCTGGG
 TTGTGCTCTTTGTAGGCAAGCAAAAGCTTGTCTACAAACGGGAAATTAGCTCACATGATTTTCATGCCCTGT
 GCCTCTACCTCTGGAGATTGTGCGGGGAGTGGGGGGAACCGGAGGAATAAGGGAAGTGGTAGTTTAACT
 AAGTTTTGTATACATGAAATCTTTCTCTCAATTAATTATCTTTAGCTTCAGAAATCTGCTCTGAGC
 CCTCTAAGCAAACTCATTAAGCAATTAAAGAGAAATCTAATTTTAAAGGTGAGCACTTTTCTTTTCTCTC
 CCACAGAGGTTGCTAATCTCATTTATGCTGTGCTATCTGAAAGAACTTAAGGCCAATTCAGCTCTCGTCTG
 GGCATTGTGATGGATTGACCTCCATTCTCGAGTACCTCCAGCTGATTAAAGTTTCAGAGTGGTATGTAGGTT
 TTTCTGAATTTTATATAGAAAAAAGTCTTTTTCACATGACAAATGCACACTCTACACAGACTCTTAGCCCTAGTA
 GTTTTCTAGCTCTGACACAGAGCTTAATGAGACTGTGACCTCTGCACTCAGAAAGAAATAGGCAAGT
 CCTGTGCTCAGATCTTAGCTCTGATTTAATAGTTGAGACCACTTACACATGCAAGATGCACTTCTCCAG
 ACTTCAAGAGTTACCATGCGAAAGGAAAGGTATTTCAGTAAAGGAAATAGTTTCTCAACCATTTAAAAAT
 CTTCTGAACCTCAAAAGTAGAAGAGCCCAACCTTTTCTCTGCTCTCAAGAGGACAGACATTTGGTATG
 ATTTAGCATCACACACATTTATGAGTATATGTAAGTAACTCAGAGGGCAATGCCACTGTTATTTATCTCCCA
 GGGTTTCCAGCAAGTACACAGACTCTCTGTTAGGATTAGGGGCCACTTGTGTTTTCGGCTTATTTTACTGCGA
 CTGTGACAGAAATGAGCGCTAGTCTATGACATGGCCAGTAGAGCAGGGCTTGTATGATCATGATGAT
 GGTAGAGGAATCATCATCATACCCCTCTCAGAGAGAAATTTACAAACAGAGAAATATCTCTTTTGG
 AGCAAGATCTCATATGTTTTCAGGAGTAGTCAAAATAAAATTAATCTCTCTAGATGAGTGGCGATGTTG
 GCTGATTTGGGTCTGCATTGACAGAAATGCAATAAAAAAGGAATTAGCTAGAATATGACCATTAATATGTGCTT
 CTGAAATATATTTTGAAGTTTGAAGATGCA

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MDFFLLGLLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLGLSLRYNSLSELRAQOFTGLMQLTWLYLDHNHICSVQGDAPQKLRRVKELTLSSNQ
ITQLPNTTFRPMENLRSVDLSYNKLQALAPDLFHGLRKLTLTHMRANA IQFVPRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRILTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLADGEGEQHDGTFE PATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVLVLYSVSKCFASLRQLRQCFVCTQRRKQKQKQTMHQMAAMSQAEEYVYDKPNH
IEGALVINEYGSTCTHOOPARECV

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGA**CTTCGACGTCGCAGCCAA**
CTGGAGCCAGAACC**GGACCCCGT**CGCGCGGCGGCGCGCTTGAGTTCCCGCGGACAAGATGG
TGTCA**GTCTCTGGT**GCAAGAAGGTCACGCGCTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCTCTGGCTTCAGGAGCCGGATTCGGCGCTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGCGCGCT**TGA**CGCTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFFADKMVSVLVQE
GHAVSDMLLPDGLVVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGLSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTC**CATG**GGACCAGTGAAACAGCTGAAGCGAATGTT
 TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTGTGTTTTGCACTTACCCCTGTGTT
 CTGCCTTTTGGTGGCATAACAAGGGACTTGCACCTTATCTTCTGCATTTTGCAGTCTTTGGCA
 TTGACGTGGTACAGCCTTTCCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGC
 CGTGTGTCTTGCAT**TAA**TTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG
 CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
 TGCAGCAATGTGTTGCTTGTGATTTCGAACATTTGAGGGTTACTTTTGGGAAGCAACAATACAT
 TCTCGAACCTGAATGTGCTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
 TCTTCCTCATGTACCTGTTTCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
 CTATTTCAGCAACAGCAA
 AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGTTCCTCCAGTCACCCCTCCGCGGTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCTCCCTCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAATTAGGGGGAGAAAGGACAGAGAGCAACTACCATCATAGCCAGATAGATTATCTTACTCTG
 AACTGATCAAGTACTTTGAAATGACTTCGAAATTTATCTTGGTGTCTCTCATACTTGCTGCACCTGAGTCTTTC
 AACCACTTTTCTCCTCACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTGATGGATTCGGTGGGATTA
 TATATAAAGTTCACAGCCCCATTTCATTATATATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTATACAAAACTTACCCTAACCATATATCTTTGGTAACCTGGCCTCTTTCGACAGAAATCATGGGATTTGTTGC
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCGAAGTTT
 GGGAGAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATAGTGGTGCAGCCATTTGGCCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATACATGCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCGCTGTCAATTCAGATATTGACAAGAACTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTTGGGAACACTCTGAACCTAATCATCACAGTGATCATGG
 AATGACGCGAGTCTCTGAGGAAAGGTTAATAGAACTTGACCACTACCTGGATAAAGACCATTATACCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGCTCATGAAGCACTAACTCAGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACAATTTACAGAAATAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTTCAGAAAGAAATTC
 TCAAAAGAGCCATGAACTCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTGACGAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCTGGTAGTGTTAAACCAGCAGAATATGACCAAGAGGGGTATACCCCTATTTCATAGGGGTCT
 TCTCTGGCAGCATATAGTGATTGATTTTTTGTATTTTCAATTAAGCATTAATTCACAGTCAAATACCTGC
 CTTACAAGATATGCATGCTGAATAGCTCAACCATATTTACAGCCTAATGTTACTTTGAAGTGGATTTGCATA
 TTGAAGTGGAGATCCATAATTTATGTCAGTGTTTAAAGGTTTCAAATTCGGGAAACAGTTCCAAATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACATACACACACAGGACCAA
 ATACTTACACCTGCAAAAGGAATAAGATGTGAGAGTATGTCTCCATTGTTCACTGTACATAGGGATAGATAAG
 ATCTCGCTTTAATTTGGAGCTTGGCCAGATATGTATATTTAGCAACTTTGCATATGTAAGTACCTTATAT
 ATTGCACTTTAATTTCTCTCTGATGGGTACTTAAATTTGAATGCACTTTAGGACAGTTATGCTCTATAAC
 TTGATTTGAATGCAACTTTTGGCACCCTATGTCACAGATACTTGTACGCATCTTCAAACCTGAAGGAATTT
 TCTAATATCCCGAATAATGAACATAGAAATCTATCTCATAAATGAGAGAAAGAGGTGATAAGTGTGA
 AAAATTAATGTATACCTTTGAACCTTGAATTTTGGAGATGATTCCCAACAGCAGAATGCAACTGTGGGCAT
 TTCTTGTCTTATTTCTTCCAGAGAACGTGGTTTTCTATTATTTTCCCTCAAAGAGAGTCAAATACAGCAG
 ATTCTCTCTAAATATATGTTTTCTGTATATAAATATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCA
 TAATAATGAGACCATGATATACCTTTCTCTATATAGTTCAGCAATGGCCTGAATAGAAGCACCAGGCA
 CAICTCAGCAATGTTTTCTCTGTTTGTATTTGCTCCTTTGAAATTAATCACTATTAAATACATTAA
 AATCAATTTGGATAAAAA

MTSKFILVSLAALSLSTTFSLQLDQQKVLVSVDFGRWDYLYKVPTPHFYIMKYGVHVK
QVTNVFITKTPNHYTLVTGLFAENHGIVANDMFDPIRKSFSLDHNNIYDSKFWEATPIW
ITNQRAGHTSGAAMWPGTDVKIHKRFPPTHYPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPVISIDIDKKLGYLIQMLKKAKLWNTLNLIIITSDHGMTQCSEER
LIELDQYLDKDHYTELDQSPVAAIILPEKGFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILHNSDDDFLLGNHGYDNALDMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSKFNWQDLLNSAMRPVVPYTQSTILLPGSVKPAEYDQEGSYFYF
IGVSLGSLIIVIVFVIFIKHLIHSOIPALODMHAETIAOPLLO

amino acids 1-22

amino acids 429-452

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

amino acids 69-85

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTCTGCTCCACGGGCGGGACCTTTGTAAGTGCAGGGAGGCCAG
 GACAGGCCCCACCTTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCTTGCCTTGGGTCACACAGCCAAAGGAGGCAGGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGACAATGGCCACCTGGGACGAAAAGGCAGTCAACCCGAGGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCTTGGAACTCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCTTGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCTGCTTGGTGGTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCACCTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTCATCTTGACATTTGCTCTCTGTTCCAGGAGACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTTCAACACGCTTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAGTCTTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAAATATGACAGAATTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELIDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVQLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCAGCAGGCCGCCAAT**AT**
GCTCTGTCTGTGCCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTG
 AGTCGAAAGGGGCTCCTCGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTATCCCCCTCC
 CAGGAATTTCTCCACTACCGCCAGTGGAGGACAGAAAATTTGTAAGCTGGAGATTAAGGACTT
 TGATGGGACAGCTAGACTTTTGAAGAATTTGTCCATTATCTCCAAAGATCATGAGAAGAAGCTGA
 GGCTGGGTGTTTAAAGATTTTGGACAAAAAAGAAATGATGGAGCGATTGACGCCGAGGAGATCATG
 CAGTCCCTGCGGGGACTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAG
 CATGGATAAAAAAGCGCACGATGACCATCGACTGGAAACGAGTGGAGAGACTACCACCTCTCC
 ACCCGCTGGAAAAATCTCCCGAGATCATCTCTACTGGAAAGCATTTCCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTTACAGTGGAGGAGAGGCAGACGGGGATGTGGT
 GAGACACTTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGACGGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATGCAAGTCCATGCTCCCGCAGCAACAACATGGGCATCGTTGGT
 GGTCTCACTCAGATGATTGAGAGAGGAGGGGCGAGGTCACTCTGGCGGGGCAATGGCATCAA
 CGTCTCAAAATTTGCCCGGAATCAGCCATCAAAATTCATGGCCATGAGCAGATCAAGCGCC
 TTGTTGTAGTGACAGGAGACTCTGAGGATTACAGAGAGGCTTTGTGGCAGGGTCTCTTGGCA
 GGGCCATCGCCAGAGCAGCTCTACCCATGGAGGTCCTGAAGACCGGATGGCGTCCG
 GAGCAAGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTCTACAAAGGCTATGTCCCCAACATGCTGGGCTCATCCCTATGCGCGGACT
 GACTTGGCAGTCTACAGAGCTCAAGAATGCCTGGCTGCAGCACTATGAGTGAACAGCGC
 GGCCCGCGCTTTTGTGCTCTGGGCTGTGGCCACTGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTACCCCTGCGCCTAGTCAGGACCGGATGCAGGCGCAAGCTCTATTGAGGGCGCT
 CGCGAGGTGACCATGAGCAGCTCTCAAAACATATCTTGGGACCGAGGGGCGCTTCGGGT
 GTACAGGGGCTGGGCCCACTTCATGAAGGTGATCCAGCTGTGAGCTCAGCTACGTGG
 TCTACGAGAACCTGAAGATCACCTTGGCGTGCAGTGCGGGTGAAGGGGGAGGGGCGCCG
 GCAGTGGACTCGCTGATCTGGGCGCGAGCCTGGGGTGTGCAGCCATCTCATTTCTGTGAATG
 TGCCAACACTAAGCTGTCTCGAGCCAAAGCTGTGAAAACCTAGACGCACCCGACGGGAGGT
 GGGAGAGCTGCGAGGCGCAGGGCTGTCTGTCTGACCCAGCAGACCTCTCTGTGTGTTCC
 AGCCAAACACCCAGCAGCTTCTTAGGTCAGGGTCAGCAGGCTCCGGCTCAGATGTGTAA
 GACAGCAATTTTCTGAGTGCCTGCCAATAGTGAGCTTGGAGCTGGAGGCGCGGCTTAGT
 TCTTCCATTTTCACTTGTGAGCAGCTGTGTGGCCAGGGCCCTGCGCTGTGTTCTGCCGTGC
 ATCTCCTTGTGCCCTTCTGCTGCTGCTGTCTGCTGAGGTAAAGTGAAGTACGTACGTGGCT
 CCCACATCCCACCCCTCTCTCAATCCATATCCATGATGAAGGTGAAGTGAAGGAGGAGG
 CCCAGGCTGACTTCCCAACTACAGCATGAGGCCAATTTGGCTGTGAAGAAAGAGGAAAG
 GATCTGGCTTGTGTGCTCACTGGCATGTGAGCCCTGCTGATGGCTGGGCTCTCGGCTGCT
 TGGGAGTGCAGGGGCTCGGGCTGCTGAGCTGGCTGGTGCACAGAAAGCAGGTCTGGGCTCA
 TGGTGTCTGAGCTGGCTGGACCTGACAGTGGGCCCCACCTCAGACCAAACTCACTG
 TCCCCATGTGGCATGAGGCGAGTGGAGCACCATCTTTGAGGCGCAAGGCAGAGCGTTTGT
 GTGTTCTGGGGAGGGAAGGAAAGGTGTGGAGGCTTAAATATGACTGTTGGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGACAAATGAGCGACTTCTGTCTTCCAGAGGAAGCAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGAGCGCTGGGGGTCTCTGTCCAAAC
 CCAGCAGGGGCGCAGCGGACAGCCCACTTCCACTTGTGCTCACTGTGGAACCTTATT
 ATTTTGTATTTTATTGTAACAGAGTTATGTCTTAACATTTTATAGATTTGTTTAAATTA
 CTTGTGATTTTCAAGTTCTTTTATTCATATTATGTTCTATGTTGATTTGATTTTCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGAGAAGGGGGCTTGGGCCCTGCAGTCACAT
 CTGTCCAGAGAAATTTCTTTTGGGACTGGAGGCAGAAAGCGCCACAGGCAAGCAGCCCTG
 GTCCTTTCTTTTGGCAGGTGTGGGAAAGGCTTGGCCCGAGCTTAGGATTTTCAGGTTTGA
 CTGGGGCGCTGGAGAGAGAGGAGGAACCTCAATAACCTGAAGGTGGAATCCAGTATTTC
 CTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTCTGAATGTCAAGGCACTGAGGTGCGCT
 CAGTGTGAATTTGTGTTGGGCGGGGCTGGAGGAGAGGTGGGGGCTGCTCGCTGCCCTCC
 CAGCCTTCTGCTGCCCTGCTTAACATGCCGGCCAACTGGGCACTCAGGTTGCACCTTCC
 ATTTCCACAGATGACCTGATGAGGAATCTCAATAGGATCAAAAGATCAATGCAAAATTT
 GTTATATATGAACATATACTGGAGTCGTCAAAAGCAAAATGAAGAAGAAATTGGACGTTAG
 AAGTTGTCATTTAAAGCAGCTTCTAATAAAGTTGTTCAAGCTGAAAAA
 AA

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FIGURE 206

MLCLCLYVPVIGEAEQTEFYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIFKFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQAQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCACGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGCATCAA
 ACTTCTGATATCGTGATACAAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGTAAACTCAAAGGCTTCTCTGTGTCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACATTTTACCACCAGATATGACCTAG
 TTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAAATGCAGCTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTAGTGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGACACCGATTTTATAAATAAACTGAGCACCTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIISIIILAGATAIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKNVQLTD
AGTYKCYIIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

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FIGURE 209

GAATTTGTAGAAGACAGCGGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCCTCCGCCGGCCTGC
 AGCGGGTTCATGAGCCGACCTGGGCCCAGCAGTTGCTACAGGAGATGAAGACCCCTCTTCTTG
 AATACTGAGTACCTGATGCCCTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCTGGCTGTGCCCATCTGTAACTCTCTGGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGGCGGACGCAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCCTTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCTGCCTTTTCTCTGCAGCTGTTTT
 GCTTCCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG
 GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCCTCTGATTTCTGCCTATTATCCCAGGAGCAGTTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC
 AACAGTCTACCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCTT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG
 AGTTTTGTAACTTCAAGTGCTGTTCACTGCGGGGATTTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTTTCCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTA CTGTGGCTGATCTGGACTATCATGGTGGCAGGTTCATGGACTGCAGAACT
 CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCAACCCATGAGGTAGCGAG
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAACAGACAAAAA
 AA

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FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQC
GSLLYLTLASTDLTAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSS
FPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCAATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG
 AATCTAATGGAACCTCCTGTGCTGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCT
 CAACGTGAGTAACGCCACCTGTGAGTTCCTGTCTGGTGAAACAAGACTCTTGAGGAGTCA
 TCTTTGAAAAGTTTGAGTGTGCAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACCT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCCTGAGGTCTGGGGCTGCACTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCCCTGCGGTGCTGACACCCTCTTTCCTGCTCTGCCCCGTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTCATTCAGTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKWCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLLALASLLLRGLLP

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FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGTGCTGAATCTGGGTCCCCGGCGCGCGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCGAG
 CTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTGGCCGCC
 ACGGTGTCCACCGCTTTAGCCGGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGAAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCAGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCCGTACCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACACCTATCAACAATGTC
 CCTGCAACCAGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCCACCATTCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAAACAAAAGTGGAAAA
 CACAA

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FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRS YRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMFWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

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FIGURE 215

CCGGGGTCGACCCACGCGTCCGGGGAGAAAGG**ATG**GCCGGCTGGCGGCGCGGTTGGTCTTGCTAGCTGGGGCA
 GGGCGCTGGCGAGCGGGTCCGAGGGCGACCGTGAGCGGGTGTACCGCGACTGCGCTACTGCATGCGCGAGAGACA
 GAATGCTCTGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAACTTACATGAGTCTAGCAGCTGGACCT
 GTCCGGGACGACTGTAAGTATGAGTGATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGGTACAAAGTGCGCT
 CAGTTCCATGGCAAGTGGCCCTCTCCCGGTTCTCTGTTCTTTCAAGAGCGCGCATCGGCCGTGGCCTCGTTTCT
 CAATGGCCTGGCCAGCGCTGGTGATGCTGTGCCGTACCGCACCTTCTGCGCAGCTCTCTCCGCCATGTACACCA
 CTTGTGTGGCCTTTCGCTGGGTGTCCCTCAATGCATGGTTCCTGGTCCACAGTCTTCCACACCGAGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCCCTCCACTGTATCCTACACTCAATCTAACCTGTGCTGGGTCAAGGAC
 CGTGGGGCTCGACACCCAGCTGTGGTCACTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACACGCGCGGCTGCCCTCAGCTGGCAAGTGGCTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGAG**TGA**AGACCTTGGAGCGAGTCTGCCCAAGTGGGGATCTGCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGGCCAGAACTCATGTGGCCAGGCCACCCCTGTTGGCCTCACCAAGCTTGGAGTCTGTTCTAGGG
 AAGGCTCCCAGCATCTGGGACTCGAGAGTGGCGAGCCCTCTACCTCTGGAGCTGAACGTGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTTCTCCCAACAGCCTCTCTCCACATCCCCAGCTG
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCGGAGACCACAGGCCTTAGGGATACAGGGGGTCCC
 CTCTGTATCCACCCCCACCCCTCTCCAGGACACCCTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTACGGCGATCTCCCATGGGACTTGGAGGACCAAGCTGCTGGGATTGGGAAGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCACAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCTGTGCTGTCTGTCTGGTGTGAGAGCTTGCACCGCTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCTGTGAGCTGGCCTGGGTGTGTGTGAGCTCAGGCCCTAGTGGCGCATGTGGAGACGGTGTGTG
 CGGGCAAGAGTGTGGCTTCAAAGTGTGTGTGTGAGGGGGTGGTGTGTGATGCTGGGTTAGGGAGACTGTG
 TGCCGTGCTGTGGCGCATGTGAGATGAGTGACTGCCGCTGAATGTGCCACAGTTGAGAGTTGGAGCAGAT
 GAGGGAATCTGTCAACATCAATAATCACTTGTGGAGCGCCAGCTCTGCCCAAGACGCCACCTGGCGCGACAGC
 CAGGAGCTCTCAATGCCAGGCTGCCCTGTGTGATGTTCCCTGTCTGCTGCCCTTTGCCCGCTTTGCCCGCTT
 CTCACAGGGTCCCAACACAAGCTGCCCTCCAGAAAGACGCCCTCGGAGCGAGAGAGGAAAATGGGATGCG
 TGGGCTCTCTCCATCTCTCTTTTCTCTTGGCTTGCATGGCTGGCTTCCCTCCAAAACCTCCATTCCCT
 GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGGAGGAGGAAGGGCGATTGAGGGAGAAGGGAGAAAGCT
 TATGGCTGGTCTGGTTTCTCCCTTCCAGAGGGCTTACTGTCTCAGGGTGGCCCCAGGGCAGGCGAGGGGCC
 ACATATGCTCTGTGCCCTGGTAAGGTGACCCCTGCCATTTACAGCAGCCCTGGCATGTTCTGCCCCACAGG
 AATAGAATGGAGGGAGCTCCAGAACTTTCCATCCCAAGGCGACTCTCCGTGGTGAAGCAGACTGGATTTTGT
 CTCTGCCCTTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGAATCGGGT
 GCGCTGCGCTAGCTCTTTTGATACTGAAACTTTTAAAGGTGGGAGGTGGCAAGGGATGTGCTTAATAAATCAA
 TTCCAAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFPSRFLFFQEPASAVASFNLGLASLVMLCR
 YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDLDLTKMDYFCASTVILHSIYLCCVR
 TVGLQHPAVVSAFRALLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
 RLPVHRKCVVVVLLQGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCTTGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCTGGA
 CT**ATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
 CTGATGGCCGCTGCTTACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAAGAAACCAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCAAA
 ACTCCAATATGAGGACAAGTTCGGAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAGGAGGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAGACGGCTCTTCCGCCCCATTGA
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC
 TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCCTTTGGTGG
 TCTTCAAGTGGTGAATATGGGCTGAACAGCACAGAGCCCCTCGTGAAGGAGTATGCTGCGT
 TTGTGTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
 GCCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
 CCTGTTTGCACCTGTGCTCCCTGCTGCGCCACTTCCCCATGCCAGCGGCAGTTCCTGAAGC
 TCGGGGGGCTGCAGGTCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
 CGCGTGGTCACTGCTCTACGACCTGGTACGGAGAAGATGTTGCGCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
 GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT
 GCCCCTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGTACCG
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
 TGCCCATTAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

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FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
 DAEVLEVFHPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPPYAQRQFLKL
 GGLQVLRITLVQEKGTVEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCCGGCTTCGCTAGAGGAAGTGGCGCGGACCTTCATTGCGGGTTTCGGTTCCCCCCTTCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTTGCCTGTCTGTGTCAGGCCCCACCCCC
 TTCCCACCTGACCAAGCC**ATG**GGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGGTTGCGG
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTATCATCTCGT
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCTCTGGCCTCTGTGGTCTGGTTCACTTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCT
 GTCTCTGTCTCTTACAGGAGGTGTTCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTATCAATATTTTGGCT
 GATGCACCTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTGACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCAGCC
 TCTTGTAAGGAC**TGA**CTACCTGGACTGATCGCCTGACAGATCCACCTGCCTGTCCACTG
 CCGATGACTGAGCCAGCCAGCCAGCCGGGTCCATTGCCACATCTCTGCTCTCTCTCTCTGTC
 GGTCTACCCCACTACCTGACGGGTTTTGCTTTGTCTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCTGGGTTACGCCAGTCACTGACTGGTGGGTTTGAATCTGCACCTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTGCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGACGGCCGACGGCAGGAGGACAGTCGGGTGAT
 GGTGTATTCCTGCCCTGCCCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACG
 GTTGCCAAGAAAAGGGAACCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTTGGTGTGATAAATACCCTAAACTGCCTTTTTTCTTTTT
 GAGGTGGGGGGAGGAGGAGGTATATTTGGAACCTCTTAACCTCCTTGGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAATAATGGTTTTAACCT
 CCTTAACCACCAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGAGTGCAGACTACCATGACATCGTAGGGAAGGAGG
 GAGATTTTTTGTAGTTTTTAATGGGGTGTGGGAGGGGGCGGGGAGGTTTTCTATAAACTGT
 ATCATTTTCTGCTGAGGTGGAGTGCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAAATTTGTAAAAA
 AA

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FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLI FGAAVSVLLQEVRFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNFWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTTCGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

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FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCTTTCCCCG
GGGCTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCCACNTG
ACCAGCCATGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

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FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCCNITCCCCGGGG
TCTGGGGGTGACATTGCACGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGGCCCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCCACTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGTTTCGGGCCCCGGCCTTC
GCGCTTTTCTGTACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

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FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATGG**CTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCCGGTCGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCTGTGACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATAAACTGAACAGAAGAATTCTGTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCGCTGTGGTCTGCAATGGCTCCC
 TGCAGGGGACTCGTGTCTGGGGAGATTACCCTTGTCGCCGCGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGATCCAGGAAACCATCCAGGCCAACTCT**TGA**GTCTAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCACTCTCTCCAGCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAAGTGAAAAAAA

FIGURE 226

MATARPPMMWVLCALITALLLGVTEHVLANNVSCDHPSENTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGP
VVCNGSLQGLVSWGDYPCARP NRPGVYT NLCKFTKWIQETIQANS

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FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCGGCGGA
 CAAGCGCAGCGGCGGAGCTGCGGGTACGTGCTGTGCAACGCTGCTGCTGGCCCTGGCTGTGC
 TGTGTGCTGTAGCTGTCAACCGGTGCGGCTGCTCTTCTGAACCAACGCCACCGCGCGGCGCAG
 GCGGCCCCACCTGTGCTCAGACATGGGGCTGCCAGGCCAACGCGCCCTGGTCACTGTGGGA
 AAGGGCGGACAGCTGCAGCTCAGACATCCTCATTGACCCGCGCTGCCCGACCTCACCGACA
 GCTTTCGACGCTGGAGAGCGGCCAGGGCTCGGTGCTGCAGCGCGCTGACAGAGCACCAGGCG
 CAGCCACGGCTGGTGGGCGACACAGGAGCAGGAGCTGCTGGACACGCTGGCCGACAGCTGCC
 CCGGCTGCTGGCGCCGAGCCTCAGAGCTGCAGACGGAGTGATGGCGCTGCGGAGCGGCGATG
 GCACGCTGGGCGAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGGCCAGGGCCACATGGCTCACCTGGTGGTGAACCTCCCTCAGCGACATCCTGGATGCCCT
 GCAGAGGGGACGGGGGCTGGGCGGCGCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGAACCGCGGCCCGGGGCTGTGCCATGGCTCCCGGCGCCGAGACTGTCTGGACGCTCCTC
 CTAAGCGGACAGGAGGACGATGGCGCTCTACTCTGTCTTTCCAGCCACTACCGGGCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGCAGCGCGCGGCTGGACGGTCTTTTCAGCGCGGGGAGG
 ACGGCTCCGCTGGAATCTTTCGCGGGCTGGGACGCTACCGAGACGGCTTTGGCAGGCTCACC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGGCTGACCCACACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGGACTTTGAGAAATGGCACGGCTGCTGCCGCTACCGGAGCTTCGGCG
 TGGGCTGTGTTCTCGGTGGACCTGAGGAAGACGGGTACCGCTCACCGTGGCTGACTATTCC
 GGCACCTGCAGGCGACTCCCTCCTGAAGCACAGCGGCTGAGCTTACCCACCAAGACCGTGA
 CAGCGACCACTCAGAGAACAACTGTGCGGCTTCTACCGCGGTGCTGGTGGTACCGCACT
 GCCACACGCTCAACTCTGAATGGGCACTACCTGCGCGGTGGCACAGGCTCCTATGCCGACGCG
 GTGGAGTGGTCTCTGAGGCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCGGTTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTTGGCCCTGCTGGTCCCTGTGCG
 CCCATCCCGAGCCCCACCTCACTCTTTTCGTGAATGTTCTCCACCCACTGTGGCTGGCGGAC
 CCACCTCTCCAGTAGGGAGGGGCGCGGGCCATCCCTGACACAGCTCCCTGGCGCGGTGAAGT
 CACACATCGGCTTCTCGCGCTCCACCGCCCTCATTTGGCAGCTTCCCTGATCTCTTGGCTCT
 TGCTGATGGGGGCTGGCAACTTGACGAGCCCACTCTGCTGGCCCACTGTGACTCGCG
 TGCTGTTTGGCGTCCCTGGCCAGGATGGTGGACTCTGCCCCAGGACCCCTCTGCCCTGCC
 GGCCAAATACCGGCAATTTGGGGAACAGAGAGCAGGGGCGACACACACCCCTGGAGTCTCT
 CTAGCAGATCGTGGGAATGTCAAGTCTCTCTGAGGTCAAGTCTGAGGCGCATCTCCACG
 CCTCCCAATGCCAACCCACCGCTTTCCCTGGTGCCACAGAAACCACTCTCCCCAA
 GGGCTCAGCTTGGCTGTGGGCTGGGTGGGCCCCATCCTACAGGCCCTGAGTCAAGATGGG
 GAGCTGCTGCTTTGGGACCCACGCTCCAAGGCTGAGACCACTTCCCTGGAGGCCACCCAC
 CTGTGCGCCCGGACGCTGGGCTTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG
 TCTAAATGAGCGCCCAACCCATCCCCAACCCAGCTCCCGGCGCTCTCTACCTGGGCG
 CGGGCTGCGCATCCCAATTTCTCTGCTCTTGGAAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGGTTTCTTGGGCTGGGGCTAGGCAAGGCTGGGATGAG
 GCTTGTACAAACCCACCAACCAATTTCCACAGGACTCAGGGCTCTGAGGCTCCCGAGGAG
 GCTTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGGC
 ATTGACCTTGGCCACTTGACCCAGGCCAGGCCCGGCGCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGGCAATGGGCTCGGGGGGACTGGGGGACAGACAGGCAACCACTGGACA
 CTTTCTTGTGAATCCTCCCAACACCCAGCACGCTGTCTATCCCACTCTTGTGTGACACA
 TGCACGCTGAGACCCGAGGCTCCAGGACACGACCAAGGACAGGCTGGAGCGGGG
 TCCTCAGCTGTCTGCTCAGACGCCCTGGACCCGCGTGGCTTACGTGAGGCGCCAGATGAGG
 CGGCTTTTCCAGGCTCTGATGGGGGCTCCGAAAGGGCTGGAGTCAAGCTTTGGGAGGCT
 GCTTAGCAGCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTTCCAAAGGACACCCGATGGGA
 GGTGCTTAGGGGCTGGGGGTTCGGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACCAATAAATTTGACTTGGCACCACTGGGGGTGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 TGTCACAGTGCCACCAGGTCATCCACATGGCGAG

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FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVRADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFRRGWDAYRDGFRLT
GEHWLGLKRIHALTTQAAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHSGMRFTTKDRDSHDSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

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FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTCTGAAGTACTAGCTACAGTACCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGCAGGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAAGT
 TTCCATATTATAATAGATGTCAACGAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCCTGTG
 TTTCTCTGTTTCAAGATCACCAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCACTCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCAT
 GTCTTCCTTACACTTGGTGAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTTTGTTGTTTTCAGTTTCACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCCTTCTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

230/330

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

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AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTGCGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCTTTTCAACGTGGCGACCAAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCAGCAATAAAGCTTGCAGGAAGNTGCAGCAT
TGGGCTGAAAACTCTGTCTGAGCTGTATAACAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCTCATNTACTATAACACACCACTCC

FIGURE 232

GCCGAGCGCAAGAACCTTCGCGAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTCCGGCTCGGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTTCCCGCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGTTCCGCGGGCCGGGGACCCGCGGTCGCGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGCGCGCAGGGCCCGTGGCCGTTGGGCATCTCCCTGGGGCTTACCCTGAGCCT
 GCTCAGCGTCACTTGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCCGCGCGCAACACCAACGCGGCGCGCCGCCCAACTCGGTGACGCCGCGAGCG
 GAGCGCGAGAAGCCCGGGCCGGCGAAGGCGCCGGGGAGAATTGGGAGCCGCGCTTGTGCC
 CTACCAACCTGCACAGGCCGGCCAGGCCGCCAAAAAGCCGTACGAGCCCGTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCAAGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCACGGGGCGCGCGGGCCCACTGGCATGGCAGTGGTGAAGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTCTTCTCTGGTGCCTGACACCCTACACCGAGGCGCACGGCTGGCACGCGCTTAACCTGG
 CCACCTCAGCCTGGCCTCCGCGCGCCACCTGTACCTGGCCGGCCCGAGGACTTTCATCGGCG
 GAGAGCCACCCCGGCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG
 CTGCAACAACTGCGGCCCACTTGAAGGCTGCCCAACGACATCTGTAGTGGCGCGCTTGA
 CGAGTGGCTGGGTGCTGCTATCTCGATGCCACCGGGTGGGCTGCATGGTGACACGAGG
 GGGTGCACCTATAGCATCTGGAGCTGAGCCCTGGGGAGGCACTGCAGGAGGGGGACCCCTAC
 TTCCGAAGTGCCTGACAGCCCACTCTGTGCGTGACCTGTGCACATGTACGAGCTACACAA
 AGCTTTTGCGCCAGCTGAATGGAACGCACGTACACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAAATACGACCATCTGGCCGTTGATGGGGACCGGCGAGCTTGTGCCCGTGGGTATT
 CCAGACCAATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTACGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTACCCCGCTGCCACTGCTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGAGCCTTGATCCGGCCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGAGGCGCGCGGCCCTCACTC
 CGCGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCAGGTCTCACTGTGCTGCTGCGCTCTAGCTGCGGCTGAGCGTGACCTGGCCCTGG
 CTCTCTTGAGGGCCTTTGCCACTGCAGCACTGGAGCCTGGTGTGCTGCGGCGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCATGCAGATGTCTTCGACCT
 GTCAAGGCCCAAGCTGGCAGAGCTGGAGCGCGCTTTCCCGGTGCCCGGGTGCCATGGCTCAG
 TGTGCAGACACCGTCACTCACCCTGCGCCTCATGGATCTACTCTCAAGAAGCACCCGCG
 TGGACACACTGTTCTGCTGGCCGGGCCAGACGCGTGTCTACGCTGACTTCTGAACCCG
 TGCCGCTATGCATGCATCTCCGGCTGCGAGCCCTTCTTCCCATGATTTCGAAGCCTTCCA
 CCCAGGTGTGGGCCCCACCAAGGGCCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCGAGCCAGCGAGGCTGCTTCTACAACCTCCGACTAGCTGGCAGCCCTGGG
 CGCCTGGCGCGCAGCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACAGCT
 GTTCTCTCACTTCTCCAGTGTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGGCCCAAGCTGACGCGCGAGGCTCAGTAGGACCTTAGGACACACCCCAAGCACTGG
 GTGCTTGAGGGCTCGGCTCCCGAACCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCAGCT**GAC**CCCCACCTGTCCCGCTGGGCGTGGGCTGGCCACACCCCAACCTT
 CTCGCCAAAACAGAGCCACCTGCCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCC
 AAGCTGGCCCACTGGTCCCTCTCTGCTCTGTGGTCTCTGGGCTGTGGAGCTGGGAGCTGGG
 GAGCGTGCCCCAGAGCAGCCCACTTCTATCCCAAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTCCGGCTGTGGCTCCACGTAATTTATGAGTACAGCTGCGCTGACGCCAGCCCTGC
 CTCGTGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGGAGGG
 GCATCTCCCAACTTCTCCCTTTTGAGACCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

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FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQLLVAVL
TSQTTLPFTLGVAVNRTLGHRLERVVFLTGARGRAPPGMVVTLGEERPIGHLHLALRHLL
QHGDDEFDFFLVPDTTYTEAHGLARLTGHLASASAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN
RRYHPALRLKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHFGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSR TQLAML LFEQE QGNST

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FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGCGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAATCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAAG
 AGGGTTGCTCAACGCCCGCCTCATTGGAACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTCTATGGCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGCCGCCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAACTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCTTGGCAGCACCTTTGTGGCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCTTGTAATACCGAGAGGCCAATGGC
 CTTCCATCATGGAATCCAACGTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTG
 ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLAAAAATRGLPAARVRWESSFSRTTVVAPSAVAGKRPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGCTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCCAGCA
AGATCCAG

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FIGURE 237

GCGGGCGGCT**ATG**CCGCTTGGCTCTGCTCGTCTGTGTCTCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCCCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCAGATTCCGCGACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCATTACACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCTTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCAGTGTGGATAAA
 TCTTGGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCACTACCACTCCCAGGCAGTGCATATCCGCCCTGTCTTGCGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGTATTTGATGCCTTC
 ATCAGGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAAACCCCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACACCAGGACA
 ACGAGACATTAGAGGTGACCCACCCCGACCACTACATATCAGGACGTCATCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCAAGAAATGAGGCCCCCAGTGCCTTCTCTGC
 ATGCCCAGCGGTAGTGTGAGTGGCTATGGGCTGCAGAAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCCCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTACAGTGCCTG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGGCGGGCGCTGCTGAAGTGGACCGAGTA
 CAGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCTCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACTGATCTGCCTCAGCTGCACGTGTGGTGGCCGTGT
 GCTACGGCTCCTTACAACTCTCCTCACCCGAACCTTCCACATCAGGAGCCCCGCGACAGGT
 GGCTTGCCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTC**TGA**TT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTGGCTTTTGAACCAAAGTGCCTGGACAGGTGAGGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAAATTTGAATTA
 CTTAGAAATTCATTCCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAA
 AGTGGTCCGGTGGCTGTATTTGGACGACAGAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAACCGCTGTTCCGTGGAAAAA

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FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPAKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKEPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSI SWELRQTLSVVFDAFITG
QGKDWLSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLLDTPWYLRLYVHTLTITISKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

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FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATTGATGCTGGGTCCCTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGAAGAGTCAAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMSLVLTSLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGAGCCACCACCA**AT**GAGGTCCTGCCTGTGGAGATGCAGGCACTTGAGCCAAAG
 CGTCCAGTGGTCTTGCCTTGTGGCTGTCTTCTTCTTCTCCGCTTGCCCTTTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCCAGGAGGACAAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCACCCGCCGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCCCAGAAAAAGAGAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGAGAGAAGCACAGGGCAAAGCGGCAACCCAGCCAAGACGCTCATTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCAG
 AGCCCCACGACGCAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTCTGCCAACCTCACTCTC
 TTCTTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGAACTTGTGCCAACG
 CTTTGGCTCATGGAGCTCAACTACTCCTTGGTGCAGAAAGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGTCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCACTCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACCTCTTATATTGGGCAAT
 CGGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTTCCCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAAGGCACAGACCCAGGAAGCTTTTCCGGGAAGCCTTGACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGTCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGTATTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGGAAGCGCTACACGTGAAGGATAATCCGGCTGTACCAGCGCTCTGGCT
 CCGGAACTGCCAAAGCAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTTTTGCCATTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTTCTGAAGTTCCTCAGTACATTGCTTAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAGAAACACTCTT
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTCTAGAAACCTTTCTAGGAGTTATCTGATTTAGAAGGGCTATACCTTGCCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAGGCAATAAATTTTCTACAGTGAACCAAAAAAAAAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAFLVFFLFALPSFIKEPQTKPSRHQRTEINIKERSLQSLAKE
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQDTKTTQGNNGGQTRKLTASRTVSEKHQ
 KAATTAKTLIPKSHRMLAPTGA VSTRTRQKGVTTAVIPPEKKKPQATPPAPPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPPGFMEELNYSVLVQKVTRFPVPVQQQLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLPDFL
 RYMKNRFLRSKTLGDAHWRIRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTATTTTTCAGACAGACTCTTCCATAAGTCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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FIGURE 244

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

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FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCGGACCCCGGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACCTAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTACTGGGGGCAAGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGT
 TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLLSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMFPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

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FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGCGCGCGCAAGGGTGAGGGCGGCCAGAA
 CCCAGGTAGTAGAGCAAGAAGATGCTGTGTTCTGCCCTCAAATGGTCCCTTGCAACCATG
 TCAATTTCTACTTTCTCTACTGTTGGCTCTCTTAACCTGTGTCACCTCTTACAGTGTGTCAGAG
 CACTGAAGCTATCTCCAAAACGTAGTGATGGGACACCATTTCCCTTGAATATAAATACGACTTC
 CTCAGTAGCTCATCCGACTTCATTATGATCTCTTGATCCATGCAAAACCTTACCACCTGACCC
 TTCTGGGGAACCAAGAGTAGAAATCACAGCCAGTCAGCCACCAGGACCATCATCTGCGCA
 TACTCACCACTGCAGATATCTAGGGCCACCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCTTCAGCTCTGGGAACCCCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG
 CCCTCTCTGTGGCTTCCCGTACACAGTTGCTATTCACTATGCTGGCAATCTTTCCGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAGGAAGGGGAACCTGAGGATACATAGCAT
 CACACAAATTTGAGCCACTGCAGCTAGAATGGCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAATTTTCAATCAAAATTAGAAGAGAGCCAGGCACTAGCCATCTCCAATATGCC
 ATTTGGTAAATCTGTGACTGTGCTGAAGGACITACAGAAGACCATTTTGATGTCACGTGGA
 AGATGAGCACTATCTGGTGGCTTCATCATTCAGATTTTGAGTCTGTCAGCAGAGATAACC
 AAGAAGCTCAAGGTTCTCTGTTTATGCTGTGCAGACAGATAAATCAGCAGATATATGC
 ACTGGATGCTCGGCTGACTCTCTCAAAATTTATGAGGATTTTACGATACCGTATCTCCCC
 TACCCAAACAAGATCTTGCTGCTATTCGGACTTTTCACTCTGGTGTATGAAAACTGGGGA
 CTGACACATACAGAAATCTGCTCTTTGTTGATGCGAGAAAGTCTTCTGCATCAGTAA
 GCTTGGCATCAGAGTGTGGCCCATGAACCTGCCACAGCTGGTGTGGGAACCTGGTCA
 CTCTGCAATCTGAATCATCTTGGCTAATGAAGGATTCGCAAAATTTATGAGATTTGIG
 TCTGTAGTGTGACCAATCTGAACCTGAAGTTGAGATATTTCTTGGCAATGTTTGA
 CGCAATGGAGTAGATGCTTTAAATTTCTCACACCCTGTGTCTACCTGTGGAAATCTCTG
 CTCAGATCCGGAGATCTTTGATGATGTTTCTTATGATGAGGAGCTTGTATCTGAATATG
 CTAAGGGAGTATCTTTAGCGCTGACGCAATTTAAAAGTGTATTTGTACAGATATCTCCGAAGCA
 TAGCTATAAAATACAAAACAGGAGCTGTGGATAGTATGTCGAAGTATTTGCCCTACAG
 ATGGTGTAAAAGGATGGATGGCTTTTGTCTAGAAGTCAACATTCATCTTCACTCTCACAT
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACATTTGGACCTTCAGAGGGGTTT
 TCCCTTAATAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGCTCTGACGGCCGCCCGGACACTGGGTACCTGTGGCATGTCCATTGACATTCATCACC
 AGCAAAATCCAACATGGTCCATCGATTTTGTCAAAAACAAAACAGATGTGCTCATCTCC
 AGAAGAGGTGGAATGATCAAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTAG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTCATTAACAATGCCATTCAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGAGGCCCTGGATTTATCCCTGTACTTGAACATGAAACTGAAATTTAGCCCGTGTTTC
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAGAGATATGAATGAAGT
 GAAACTCAAATCAAGGCCCTCTCATCAGGCTGCTAAGGGAGCTCATGTATGAAGCAGCATG
 GCAGACGAGGGCTCAGTCTGCAGAGCAAACTGCGGAGTGAACTACTACTCTCGCTCTG
 TGCACAACTATCAGCGGTGCTACAGAGGGCAGAGGCTATTTTCAGAAAGTGGAAAGGAATCC
 AATGGAAACTTTGAGCTGCTGTGCGACTGACCTTGGCAGTGTGTTGCTGTGGGGGCCAGAG
 CACAGAAAGGCTGGGATTTTCTTATAGTAAATACAGTTTCTTGTCCAGTACTGAGAAA
 GCCAAATTTGAATTTGCCCTCTGCAGAACCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATCTTACACTATTGG
 CAGGAACCCAGTAGGATAGAACTGGCCACTGGCCTGCAATTTCTGAGGAAAACCTGGAACAAATGG
 TACAAAAGTTTGAACCTTGCTCATCTTCCATAGCCACATGGTAATGGGTACACAAATCAA
 TTCTCCACAAGAACCGCTTGAAGAGGTAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAATTGAACCATTTGAAGAAACATCCGTTGGATGG
 ATAAGAAATTTGATAAAATCAGAGTGTGGTGCAGAAAGTGAACGTATGCTAATAA
 CTAGCTCCCTTGCCCGGTTCTCTTATCTCTAATCACCACATTTTGTGTAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTGGCTCCAACCTGGAGTACTTTTCCCTTCACTCATTTTGTGA
 CTATCCCTGTGAAAGAATAGCTGTAGTGTATTTTTCATGAATGGGCTTTTTCATGAATGGGCTA
 TCGCTACCATGTGTTTGTGTTTCTATCACAGGTGTGGCTGCAACGTGAACCAAGCTGTTGGGT
 TCCTGCCACAGAAGATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFFWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
 HPPQEQIALLAPEPLLVLPTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSSTYLVA
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLFEFYEDYSFIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELA HQWFGNLVTMEWWDNL
 WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGDMG
 FCSRSQHSSSSSHWHQEGVDVKTMMTWTWLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLFKTKTDVLILPEEVEWIKFNVMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKMRDMNEVETQKFAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTESKQIEFALC
 RTQNKELQWLLDESFKGDKIKTQEPFQILTLIGRNPVGYP LAWQFLRKNWNKLVQKFELGS
 SIAHVMVGTTNFQSTRTLRLEEVKGFFSSSLKENGSQLRCVQQTETIETIENIGWMDKNFDKIR
 VWLOSEKLEMM

amino acids 1-34

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACACAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGACCACCATATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCAGCATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCACTTCTGTCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACAAATCATTCATATCTACTCACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

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FIGURE 250

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEP RVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSVLLN
SLPPQAAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC
PSC

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FIGURE 251

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
 CAGG**ATG**AGGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCCTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCGTCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGAGCGGCTTGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGCAT
 GGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**CGCCTCAGGCTGGGGGTGCCATTGGGGGCCCCACATGTCCTTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E F G L P C E C S Q L R K A I G E
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N
G L M A A Y L A Q A G L A R V F T G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S
G G W N D V A C H T T M Y F M C E F D K E N M

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FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGACAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGCTGTGAAGGAGCCACAGGAGGAGGTGG
 TTCTTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCC
 CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTAGAGTTCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSGFVAVCKPEQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEORPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCCGTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGGCCATGAGCTGCGTCCTGGGTGGTGTGTCATCCCTTGGGGC
 TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCCAAGGCTGGTCTGAACTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCAACCCTGTCTGGCTCTGGCTCTGTTCTTAAACATTCTGCCAAA
 ACAACACACGTTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTACATGTCACTCTTGGTAGC
 TCCACTGGGAAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
 CTTAGCCCCGTGTGAGCCTCACTTTCACCTTGGAGAGTCTTCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAAGTCAACCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAAA

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FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

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FIGURE 257

AAGGAGAGGCCACCGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTTGTCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGAC**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

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FIGURE 258

MGSGPLVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

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FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
 CAAAAACAACAGACTAGTACTCTAAGAAGCTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
 TATTAATATTTACCATTCGAGAAGCTTCATTCAAGTGTGAAAATGAATGCTTAGTGGATCTG
 TGCCTCTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC
 CTCCGATTGTTCTAAATTAATGAAAGATGTCTGCTGTGAAAAAGGCATGATTTAAATCTG
 TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTT
 TTTTCTTGGCCTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
 GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
 ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAATATTACTTCAT
 TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTGCATTTTCTC
 AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGCTCTCTACTA
 TCTTCAGATTACTTGATTCAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
 ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP

SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTGGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAAGACTGCCCTGCTTGGTGTTTTGAGGAGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTCTGTTCCTTGCAGCTTTTCTGCCCCGCGCCGAGGTGAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAAGCGCTTTCGAGTCTTGAGAGCAAGGGCTGG
 AAAAAATGATACCCAAGCAAGCAGGGGCATACATTCAAGAAATCCAAGAGTTCTCAAAAAATATA
 TCTGTCTCATGCTGGGAAGATTCTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCAGTGAAGTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG
 ACCGATGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAAGCTGAAGAA
 GAGAAAAAGATCCGAGCTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTTATTAAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGGAAGCAAAATCCTAACACTTTC
 CTGGCAGGGAAACAGGCCAAGTGATCTACAAGGTTTTCTATTTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCTGCAGAAGAGGAGCTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCACCCATAGCCATTTGGTCTCTCA
 CAAAGATTGAGCCGGCAGCACTGGGAGTGGAGCATTTCATGGGATACCCCATGCAAGAAGCCAG
 GATGCTGAAGCCTCATTCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACATATCAGTGAGGAGGACTTGC
 CCAACTTGTCTCTCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCTGGAATGAAGGAACAGAGTCATTACAAAATCCAGACAAGAGAGAA
 GCTGCCCTCTGAAGTAAATGCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCTTTCACAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGAATAACGTATGCCTCTCTCCCAATATGCTGCTTGGTATCTTCTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAATGTCCATTACTCCCCCAA
 CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGCTACTTCAAGCCTTTTGGTTTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTCCCTCCCAAAATAGAGTTGTATGCCAGC
 CCCTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTTCTTT
 CTTTTCTTTTTCTTTTTTTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAAATACTATTCTTATTGAGTTTAACTCTATTTCCTTAGCCCTGTCT
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAATATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTTTGACATCATTTGAATTTCTCGTTTCACTTTTGTGAACATGCAACAAG
 TCTTTACAGCTGTCTATTCTAGAGTTTAGGTGAGTAAACAATACAAGTGAAGATACAGC
 TAGAAAAATACTACAAATCCCATAGTTTTTCCATTGCCAAGGAGACATCAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAAGCCTAAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTCATGCTGCACAAGACCTTTCAATAGGCCCTTCAAAATGATAATTCTCTCC
 AGAAAACCAAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTTGTCTGTCTGTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKKIRITLLNASCDNMLMGIKSLKIVKMMMDTHGSMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWSWGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPSSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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[illegible]

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPPK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHCLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTITTTGCCTTACCCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACGTGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTCGGAGTGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCTTGCTTGCCCCAACCTGCTGTCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTT**TAG**GCCTTGCCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTCTTGCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATCCCCCTCCCCTCCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCCAAGGCAGGTGTAGGGAGCCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCCGGCGTCGGGGCGGTAAAGGCCCGGCAGAAAGGAGGCACCTTGAGAAATGTCCTTCTCCTCCAGGACCCAAAGTTTCTTCCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTGCTGCCTTGGCATTGTGTGCTTGCCAAACACAGACGTGTTTCTGTGCCAAGCCCCAGAAAGCGGCCCTGGAGTACCTTGGAGGATATAGACCTGAAAACTGGAGAAGGAACCAAGGACTTTCAAA

GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCTCTGTGCGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCTCTAGTCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTTCAAAGGAGAAATCTCTCTGGATGAAAGAAAAAGTACTTATGGTCCACAAGCGGGAATGATGTTTATGGGATTTATCCGTCTGGGAGTGGTAGCAACTCTCCGAGCCTGGAACGGAGGCTTCTCTGGAACCTGGAAAGGAGAAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCAGGAAAGCAGGGCATTTCTTCTTGAGCACCGAGAAAAAGAAATTTGGAGACAAAGTAAACCTACTTCTGTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAATGATGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATTGTTCCACTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTCTACTCTCAGTATGGATTAATAATGTATTTAATATCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAATTGACTGCCAGGCTGGGTGCAGTGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAAGTGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGCTCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGAGGACTGAGGCAGGAATCACTTGAACTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCACCACTGTATTCCAGCCTGGGTGACTGAGACTTAACATAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEGFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQLASEKK

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FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACC CGCACCCAGCCC**ATG**GCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSTSSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTCT
ATCAAGAAATAAGAGAAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATGGGGT**TATTAGAGGTTTGTGTTTCTCTTACTGTTCT
 GTGCCCTGCTGCACCACTCAAATACCTTCCCTCATTAAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTCATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTCAA
 TGATCTATATTAATTCCTGAGAAATGGAAAGGAAATCTCAGTACAAAGGGCCAAACATG
 AAAACCCATAAACATGCTGATGTTATAGTTGCACCACTTACACTCCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTTACAGAAATGTGGAGAGAAAGGCCAATACATTCACTTACCCTTGACCT
 CTTACTTGGAAAAACAAATGAATATGGACCAACCGCAAACTGTTTGTCCATGAGTGGG
 CTCACTCCCGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGCTAAG
 TCAAAAAATCGAAGCAACAAAGGTTTCCGCAAGTATCTCTGGTAGAAATAGAGTTATATA
 GTGTCAAGAGGCGAGCTGTCTTAGTAGAGCATGCAGAAATGATTCTACACAAACCTGTATG
 GAAAAATTTGTAATCTTCTTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATCTGTGTTGTTGAATTTTGTAAACGAAAAAACCCATTAATCAGAAGCTCCAAG
 CCTACAAAAACATAAAGTCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTAAAAACACCATACCCATGGTGACACCACTCTCTCACTCTCTCTCATTTGCTGAGGATC
 AGTCAAAAGATTGTGTGCTTAGTTCTTGATAAGTCTCGAAGCATGGGGGTGAAGGACCGCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACATGTTGAATAATGGATCTGGG
 TGGGGATGGTTCACCTTTGATAGTACTGCCACTATTGTAATAAGCTATCCAAATAAAAGC
 AGTGAATGAAGAAACACACTCTGGCAGGATTACTACATATCTCTCTGGGAGGAATCTCCAT
 CTGCTCTGGAATTAATATGCAATTCAGGTTGTTGGAAGCTTACATTTCAACTCTGATGGT
 CCAAGTACTCTGCTGATGATGGCAGGATACACTGCAAGTCTTGTATGATGAGATG
 AAAAAGTGGCGCATCTGTCATTTTATGCTTTGGGAAGAGCTGCTGATGAGCAGTAAT
 AGAGATGAGCAGAGATAACAGGAGGAGTCAATTTTATGTTTCAGATGAGCTGAGACAAATG
 GCCTCAATTAATGCTTTTGGGGCTCTTCACTCAGGAAATACTGATCTCCCGAAGTCCCTT
 CAGCTCGGAAGTAGGGGAATAACACTGAATAGTAATGCTGGATGAACGACACTGTCTAAT
 TGTAGTAGACAGTGGGAAGGACAGCTTCTTTCTCATCATATGCAAGCAGTCTGCCCTCCGATA
 TCTCTCTCTGGGATCCAGTGGGAACAAATAATGAAATTTTACAGTATGCAACTTCCAA
 ATGGCCCTATCTCAGTATTCAGGAACCTGCAAGAGTGGGCACTTTGGGCATACAACTCTTCAAGC
 CAAAGCAACCCAGAAACATAACTATACAGTAATTTCTCGAGCAGCAATTTCTCTGTG
 CTCCAATCACAGATGTAATGCTAAATGAATAAGGACGTAAACAGTTTCCCGACGCCAATGATT
 TTTTACGAGAAATTCATAAGGATATGTTACCTGTCTTGGAGCCAAATGTGACTGCTTTCAT
 TGAATCACAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAATGGCAGATAT
 AGTCTAAAGATTTGGGCTCATGGAGGAGCAAACTGCCAGGCTAAATTTACGGCTCCACT
 GAATAGAGCCGCGTACATACCAAGCTGGGTAGTGAACGGGAAATGAAGCAAAACCCGCCAA
 GACCTGAAATTTGATGAGGATACCTCAGACACCTTGGAGGATTTACGCCGAACAGCATCCGGA
 GGTGCATTTTGGTATCACAAGTCCCAAGCTTCCCTGGCTGACCAATACCCCAAGTCA
 AATCACAGACCTTGATGCCACAGTTTACATGAGGATAAGATATTTCTTACATGGACAGCCAG
 GAGATAATTTGATGTTGAAAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTTCTT
 GATCTAAAGAGCAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGA
 GGCCAACTCCAGGAAGGTTTGCATTTAAACAGAAATAATCTCAGAAGAAATGCAACCC
 ACATATTTATGCAATTAAGATATAGATAAAAGCAATTTGACATCAAAAGATTTCAACATTT
 GCACAGTAATCTTTGTTTCCCTCAAGCAATCTGATGACATTGATCTACACTCTCC
 TACTCTTACTCTCTCTGATAAAAGTCATAATTTCTGGAGTTAAATTTTCTACGCTGGTAT
 TGTCTGTGATTGGGTGTTGTAATTTGTAACCTTTTAAAGTACCACTT**TGA**ACCTT
 ACGAAGAAAAAATCTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAGT
 AAAGGATTTTCTGAATCTTAAATTCATCCCATGTTGTGATCATATAAATCATAAATTAATTT
 TTAAGATGTCGGAAGAGGATCTTTGATTAAATAAAACACTCATGGATATGTAAGAACTGT
 CAAGATTAATTTAATGACTTTCAATTTATTTTATTTGTAAGAAATGATGATGAAC
 AAAGATCCTTTTCACTGATACCTGGTTGTATATTTATTTGATGCAACAGTTTCTCGAAAT
 GATATTTCAAATGTCATCAAGAAATTAATAATCATCTATCTGATGATGCAAAATCAAGTAAA
 GGAGAGCAAAATAACCAACATTTGGAAAAA
 AA

MGLFRGFVFLVLLCLLHQNSTSFIKLNNGGFEDIVIVIDPSVPEDEKIEIQIEDMVTTASTY
LFEATEKRFFFKNVSILIPENWKENPOYKRPKHENHKHADVIAPPTLPGRDEPYTKQFTEC
GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQFFYRAKSKKIEATR
CSAGISGRNRVYKQGGSCLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
LDKSGSMGGKDRLNRMNQAAKHFLLTQTVENGSSWGMVHFDESTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSCSGIKYAFQVIGELHSQLDGGSEVLLLTGDGEDNTASSCIDEVQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSNGTDLSSQSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNLSLPPSISLWDPSTGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTIITVTSRAANSSVPPITVNAMKNKDVNSFPSPMIVYAEILQG
YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYSLKVRAGH
GANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFFVSQV
PSLPLPDQYPPSQITDLDATVHEHDKIILTWTAPGDNFEDVGKVKQRYIRISASILDLRDSFDD
ALQVNTDILSPKEANSKEFAFKPENISEENATHIFIAIKSDKSNLTSKVSINIAQVTLTPIF
QANPDDITDLPSTPTPTPTPKSHNSGVNLSITLVLSVIGSVVIVNFIILSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGAAACCCCTGGGAGTAGAGTACTGACAGCAAAAGACGGGAAAGACCATAACGTCCCCG
 GGCAGGGGTGACAAACAGGTGCTCATCTTTTGTACTCGTGTGTGGCTGCTTCCTTATTTCAAGGAAAG
 ACGCCAAGGTAAATTTTGAACCAAGAGGACCAATGATAGGCCACCTCCTAACTTCCTCTTCTGAAGC
 CCCAGTTATGCCAGGATTTACTATAGAGAGTGTCAACTCAACACAGCAAGCGGCTCCTTCGGCTTAACTT
 GTGGTTGGAGGAGAAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGTCCAGAGTGAATTCGCTGGA
 GGGTGGACCAGAAAGAAAGGAAGGTCCCTCTTGCTGTTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATTGAAGTGAAGAACTTGTGAGATTTTCACTTCAGTCACTGTCTGCCTGCAAGATCATCTTTTAAAA
 GTAGAGAAGCTGCTGTGTGTGGTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAATGATG
 CAAGCAGCTCCGGGGGCCCAACAGCATGCTTCCTGTGGTCTAGCCAGGGAAGCCCTCCGTGGGG
 GCCCGGCTTTGAGGATGCCACCGGTTCTGGACGATGGCTGATTCCTGATGATGATGGTTCGCC
 GGGGGTGCCTTGGCTGGATTTCCCGGGTGGTGGTTTGTGCTGGTGCCTCCTGCTGTGCTATCTCTGT
 CCTGTACATGTTGGCTGCACCCCAAAAGGTGACGAGGAGCAGTGGCAGCTGCCACGGGGCCCAACAGC
 GCCCGGGGAAGGAGGGGTACCAAGGCGTCTCTCAGGAGTGGGAGGAGCAGCAGCCGAACCTACGTGA
 GCAGCTGAAGCGGCAGATTCGCACAGCTCAAGGAGGAGCTGCAGAGAGGAGTGAAGCAGCTCAGGAA
 TGGGAGCTACCAAGCGCAGCAGATGCTGCTGGCTGTGACAGAGGAGCCCAAGAGAAACCCAG
 GCGACCTCTGGCTTCTCTGCATCTCGAGGTGGACAAGGCAGAGTGAATGCTGGCTGCAGCTGG
 CCACAGAGTATGCACAGTGGCTTTCGATAGCTTACTCTACAGAAGGTGTACCAAGCTGGAGACTGG
 CCTTACCCGCCACCCCGAGGAGAAGCTGTGAGGAAGGACAAGCGGGATGATTTGGTGAAGCCATT
 GAATCAGCCTTGGAGACCTTGAACATCTCTGACAGAGACAGCCCAATCAGCGTCTTACACGGCCT
 TGTATTTCTATAGAAGGATCTTACCGAACAAGAAAGGGAACATTTGATGAGTCACTTCTCAA
 AGGGGAGCAACAAACAGCAATTTCAAACGGCTCATCTTATTTGCAGCAATCAGCCCCATCATGAAGTG
 AAAATGAAAAAGCTCAACATGGCCCAACACGCTTTATCAATGTTATCTGCTCCCTTAGCAAAAAGGGTGG
 ACAAGTTCCGGGAGCTTGTACGAGAATTTCAAGGAGATGTGCATTAGCAGGATGGGAGAGTCCATCT
 CACTGTTTGGTACTTTGGGAAAGAAATAAATGAAGTCAAAGGAATTTTGAAGACACTTCCAAA
 GCTGCCAATCTCAGGAAGTTTACCTTCATCCAGCTGAATGAGAATTTTCTCGGGGAAAGGGACTTG
 ATGTTGGAAGCCCTCTCTGGAAGGGAAGCAACGCTCTCTTTTCTGTGATGTGACATCTACTT
 CACATCTGAATTCCTCAATACGTGAGGCTGAATCAGCAGCCAGGAGAGAGATTTTATCCAGTT
 CTTTTCAGTCAGTACAATCCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGAACAGC
 AGCTGGCTATAAAGAGAAAGCACTGGATTTGGAGAGAACTTTGGATTTGGGATGACGTGTCAGTATCG
 GTCAGACTTCATCAATATAGGTGGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCCGTGTGCAGGACTCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCTAGCAGTCCAA
 GGCCATGAACAGGAGCTCCACGGCCAGCTGGGCATGCTGGTGTTCAGGCGCAGATAGAGGGCTCAC
 CTTTCGCAACAGAAACAGAGACAGTAGCAAAAAAACA**TGA**ACTCCACAGAGAAGGATGTGGGAGA
 CACTTTTCTTCTTTTTCGAATTTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGGAGC
 ACATAAAGATTTGGACTGATGGGTGAGAGATGAGAAGGCTCCGATTTCTCTCTGTGGGCTTTTAC
 AACAGAAATCAAAATCTCCGCTTTTGCCTGAAAAGTAAACCGATGACCTGTGAAGTGTCTGACA
 AAGCAGAAATGCTTGAGATTTAAGCCTAATGGTGTGGAGGTTTGTGATGGTGTGTACAATACACT
 GAGACCTGTTGTTTGTGTGCTATTGAATATTCATGATTAAGCAGCTTTGTAAAAAATTCAT
 TAGCATGAAGAAGCAAGCATATTTCTCTCATATGAATGAGCCTATCAGCAGGCTCTAGTTTCTAGG
 AATGCTAAAAATACAGAAGGCAAGGAGAGGAGATAGGCTTATTATGATACTAGTGAGTACATTAAGTA
 AAATAAATGGACAGAAAGAAAGAAAGAAACATAAATATCGTGTATATTTTCCCAAGATTAACCA
 AAAATTAATCTGCTTATCTTTTGGTGTCCCTTTAACTGTCTCGGTTTTTTTCTTTTATTTAAAAAT
 GCACITTTTTTTTGTGAGTTATAGTCTGCTTATTTAATACCATTTTCACTATGACAGAGA
 GCACAAGTTGGGCTACATTTTATATTTTTTAAGAAGATACTTTGAGATGCATTTGAGAACTTTCA
 GTTCAAAGCATCAATTTGATGCCATATCCAAGGCATGCCAAATGGCTGATCTGAGGCACTGAAT
 GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGACGTACAGATATCTTCTGTGA
 GAGTATTTTTCGAGAGGAGCACTGAACACTGGAGGAAAAGAAATGACACTTTTCTGCTTTACAGA
 AAGGAATCTATCAGCTGGTGATATCGTGATGTACCTAAAAGTCAGAAACACACATTTTCTCCTCA
 GAGTAGGAGACCTTTCTACCTGTTAAATAAACCAAAGTATACCGCTGACCCAAACAACTCTCT
 TTTCAAAACAGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 ATATATATATATGTTGAAAGATCAATCCATCTGCCAGAACTGATGGATGGAGTTTCTGTACTAT
 GTTATCAACCCCAAGCGAGGTGGAAGTAACTGAATTTTAAATTAAGCACTTCTACTCAATCA
 CCAAGATGCTCTGAAATTCGATTTTATTACCATTTCAAACATATTTTAAAAATTAATACAGTTA
 ACATAGAGTGGTTTCTTCATTATGTGAAATTTATTAGCCAGCACCAGTGCATGAGCTAATATTCT
 CTTTGAGTCCTTGCTTCTGTTTGTCTACAGTAACTCATTTTAAAGGCTTCAAGAACATTAACG
 GTTGGTGTGTTAAAAAATGCATGTATTGATTTGTACTGGTATTTTGAATTTAATTAACAC
 AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVVKDKRDELVEAIES
ALETNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMAN TLIN VIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKCMQMS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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FIGURE 277

GAAAGA**AATG**TTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCAT**TGA**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCCTGCTTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGTAAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACCACTGAAATCATAAGCTATTCACGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAATGGATCCTTTTGGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAGTCCAATCTGTGCTAACCTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

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FIGURE 278

MLWLLFFLVTAIHAE LCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

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FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**CATGT**
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAAATGCACCTTCTCCAGCTTTGCCCCGTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTTAAGGACCGGTGCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCACTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTTGCCCTTAA
 GACACTACTTACAGTGTATGACTTGTATACACATATATGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTACATTTCCCTTTCACGTATTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCCTTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATTCAAACTGTAAATGACATTTTTATTTTATGTCTC
 TCCTTAACATATGAGACACATCTGTTTTACTGAATTTCTTTCAATATTTCCAGGTGATAGATT
 TTTGTCTG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIVIVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKVSVYLEDTD

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FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTTT
ATCCAACACTACTTACCTTGCCTACGATATCCCCCTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAFADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDL PNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTGCTGGTTAACAAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTGGGTGAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGAGTCCACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGT**TAA**AACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTA**AA**ACTGAGAAAT
 GGGCCGGGCACGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
 GCAGGAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPFVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
 GACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
 CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAACCTGAG
 GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

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FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCTGGACCAGACCACCAGCCACACATCCAGATTAAAGGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGATCAAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCCTTGAAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAAGTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCAGGAACTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCATAGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTTGACGTCAACGGAATCGTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTGTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCGTGCGCAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAA**ATAG**TGCTTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACITATTAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTCTCTCTAGTCTTTCTCACTTGTAACAAACCCAGTTTGTTTTCAAA
 AAATCAGAGTAGCAATGCAACTCATCACTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTCAGCCCATTAACCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCAGCCGAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTCATTCCCAACCATTGCAATTACAACCTCTAACTTAAATGGGTAACCCCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGAAAATTGCATACGCTCTGTGCAATT
 TTTTATCTGCCTAGTGCTATTCTGCTTGTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAAGCAAACAATTTT
 AAATATATTTTGTCTCTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTGCAAACTTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAGCCTGAATTCGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRS LPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
 CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTCTGCA
 GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
 GAGTCGGCGGCGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCTCAACCCGCT
 GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAAGT
 GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
 GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
 CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGCGCCCT
 CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVLVGSAPVAPVAALESAAEAGAGTLANPLGTINPLKLLLS
SLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALLGALTVEG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCCTCCGAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCCTCCGCTCCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTGAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAAGGCCCTGAAGCCCACCAAG
 CCGGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGCCCTCTCCCGCAACCTGGAAGT
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAACCT
 GTTTGATGAGATTAATCCTGAAACCAAATTAATCTTTGTTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCATTTGACCTGTCTTACCCGAAGTCGACACTTTCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCATGATGTACGGTGCAGGCAAGTTTGCTCCACCTTTGACAAGAA
 TTTTCGTTGTGCATGTCTCAAACCTGCCTACCAAGGAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAGAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC
 TGCTTATTTCCATGCCTCCTGTGCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTA**TA**ATTCAAG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAGGGGGAGAATTCA
 CATCTCTGGGTGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAAGTGTTTTGAGCCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCTGGATAAGGGAGGACTACTACAAA
 GCATTAAATTGATACATATTTTTTAAAAA

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGAC**ATG**AG
 GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
 CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
 GCCTGGGGCGCCCGTGTGTTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTTCCC
 TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCA
 TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCGGTCTCTGAGTCCC
 GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
 CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
 TCTACCACCCCA**G****TAG**GGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
 CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
 AAAAAAAAAAAAAA

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTGC
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCAATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCCTATGGCCAGCGGGAATCACTGCGGGGATT
 TGTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTGTCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTCAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEGKCWTDNGFVIPVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGACTCTGCCCTCGGAACAATGGGACTCGGCGCGGAGGTGCTTGGGCCG
 CGTGCTCCTGGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAAACAACAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATT
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGGAAATCCATGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTTCAAGGTAACAAGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAAGTCTGAAGCATAAATTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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FIGURE 298

MGLGARGAWAALLLGLTLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

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FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACGCTGGGCCCCAGCGATGCGGACCCCTGTGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCCCTGGCGCTTTCCGTGCTGCTGTGGC
 GCAGCTGTGAGACGCCCAAGAATTTGAGGATGTGAGATGTAATGTTATCTGCCCTCCCT
 ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACTGCTGAACAAGGTAG
 AATATGCACAGCAGCCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAGGTTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAAATACCTTGTGATTTTACCAACT
 GTTGCTGGAAGATTCAAAAGTGAAGCAAAAGTGTGCTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCATTTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTG
 TTGTTGTTGTTTTTGTGTTGTTTTGTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGAGCCAGCCTCATCAAAGAGTGACTTACTCATTTG
 ACTTTTGCACGTGACTGTATTTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGAT
 CTAATAATGCCTGGTGGCTTTTCAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTGTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCCTTTT
 TCTTCCTATGTCTCTTTTGGAAATGTAACAATAAAATAATTTTTTGAACATCAA

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FIGURE 300

MATLWGGLRLGSLLSLSCLALSLLLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHIYNKNIS QKDCDCLHVVEFMPVRGPDVEAYCLRCECKYEERSVTIKVTII
IYLSILGLLLLLYMVYLTLEV
EPIILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYA
QQRWKLQVQEQ RKSVFDRHVLS

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTCAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG
TTTACTCAATGTTTAAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTGCCCACTGAAACATCATCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCCTGAATGACTTGAATGTTTCCCCGCTGAGCTAACAGTCCATGTG
 GGTGATTACAGTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAGAT
 AGACTGGACTCTGTCAACAGGAGACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCGCAATGACGGTTCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACTT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGAAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCCTGTGTGTGTCCTGGGCCACTCTACCAGTGATTTAGACTCCCGCTCTC
 CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCAAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEEPSEKSEATYMTMHPVWPSLR
SDRNSLEKKSGGGMPKTQQAF

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FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACCTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
 GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCTATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGCTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAATGCACCCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRVMAILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL
EDGKGNMNCAYFHNGKMHPFCENKHVLMCERKAGMTKVDQLP

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FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGACCCG
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCAGTGC GGAGAA
 GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGCGCGCGGTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT
 CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACCTGTACACCTCGGAACTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAATAATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
 GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAAACAGAACCTTACCTCCAGGTGCTGTGAAT
 TCTTTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAACAACAAGCAG
 CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTTCTGAGACATATTTTGGGGGGATTTTCACTGAAAAAAGTGGGGGATCCCC
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGCTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAAGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCGGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGGAGCCGGCCGGTGTGCG
 CGCAGCGGCGCGTGTGTCCCGCGGCACCAAGTCCCTTTGCGAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGGCGCCCCGCGCGGCCGAGCCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTCTACCGCCAGCGTCGTTCTTGCCGGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCTATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCTCGAAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCACTGAGCCAGCCACCACCACAACCTGT

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FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTAAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACAT**TAG**

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FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWRPSASRRRSSPSKRNGLCNGNLVDIFSKVRIFGGLKKRRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYVYIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSCTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

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FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAT
 GAAGGATGACGAGCGACGCTTCTCCTGGAACGACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACCCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAAATAAATACTCTAAAGCAGCTGTTCCTC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAAAAGAAAAAGTATGTTCAATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAGAAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACACCTGGATTTCCTATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCGATAAATTTATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAGCAACAGTTACGCAAGGTGATTTGTGTTGCGAAAACTCGCTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCAGTTGAG
 GCATTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATGAAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTGTCTAAA
 CTGAAGGAGCTCTGGTTCGGAACCAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAAGAAATTCCTTCTTT
 GCGCCGACTAGACTTAGGGGAATTTGAAAGACTTTCATACATCTCAGAAGTGCCTTTGAAGTCTGTCCAAC
 TGAGGTATTTGAACCTTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACATGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTTCCAGGGTTTGTATGCACCTTCAAAACT
 GTGGATGATACAGTCCAGATTCAAGTATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGACATCATAGAGCGGATACAT
 TTACATCAACCCCTTGAAGCTGTAACCTGTGACATCTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCGCCGTGTAACACTCCTCCCACTCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTTCATATGCTATGCTCCGGTGTGTGGAGCCCCCTCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAATGGAACAGTCATGACACA
 TGGGCGTACAAGGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCAAAATGTAACCTGTGCAAGATA
 CAGGCGTACACATGTATGCTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCTGATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
 GACCACAGATAACAATGTGGGTCCCCTCAGTGGTGCAGTGGGAGACCACCAATGTGACCACTCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAACCTTCACCATCCAGTGACTGATATAACAGTGGGATCCAGGAATTT
 GATGAGGTACAGAGCTATGCTACCAAAATCATCATTGGGTGTTTTTGGGCCATCACACTCATGGCTGCAGTGTGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCCATGGAAAGCCACTGCCCATGCTGCTATCAGCATGAG
 CACCTAAATCACTATAACTCATACAATCTCCCTTCAACCACACAACACAGTTAAACAATAAATCAATACA
 CAGTTCAAGTGCATGAACGTTATTGATCCGAACTGAAAGCAATGTACAAGAGACTCAAAATCTAAACACA
 TTTTACAGAGTTACAAAACCAACAATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGCTTTTCAAAAAACAAAAAGAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAACGACACAAAA

FIGURE 314

MLNKMTLHPQQIMIGFRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSCSCSNQFSKVIC
 VRKNLREVPDGI STNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTINFTNVTVDQTMGYTCMVNSVGN
 TTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTVTTSLTPQ
 STRSTEXTFTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHNTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCGGGCTCCCGCCCGGCACAT
 GGGTGCAGCCACCTCGCGCGCACCCGAGGCGCCGCGCCAGCTCGCCCCAGGTTCCGTCGGA
 GCGCGCCGCGCGCCCCGCGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGG**ATG**TCCCTCCTCTCTCTCTTCTTGTAGTTTCTCTACTATGTTTGAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAACTTGACTGAGGAACAGAAGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGTACACCTGTAAGGTTAAGAATTCAAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAAGAGGAGAGGATGAACGCTGCCTCCCAAATCTAGGATT
 GACTACAACCCACCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCCTACTCTGGACTGTA
 CCAAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAACCTGTACAGT
 ATGTACAAGAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCCTCACTCGCTCCACAGCAAAAT
 AGTGCCCTCACGCAGCCAGCGGACACTGTCAACTGACGAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCCAAAGTAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGGAGCAGGACCTTCCAA
 ACGGTCT**TGA**ATTACAATGGACTTGACTCCCACGCTTTCTTAGGAGTCAAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGACGGAAACAGATTGAGATGAGCATTTTCTTATACATACCAAAACAAGCAAA
 AGGATGTAAGCTGATTCTCTGTAAAAAGGCATCTTATTTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTTG
 AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAATT
 TTCAAGAGGAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTGACAGCTCAAGCAGAAACCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAAC
 TTCAATTGTGCATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGCCCAAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
 ATGAGGATTGTTGACAAAACATTAGAATAATATAATGGAGCAATTTGGATTTCCTCCCAAT
 CAGATGCCTCTTAAGACTTTCTGCTAGATATTCTGGAAGGAGAAAAATACAACATGTCAAT
 TATCAAGCTCCTTAGAAAGAATTCTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATG
 CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAAATGTGAACCCAGAATTGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTLTGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

09989733-11004

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCCGCGGCCACGGCAGCGCAGCCA
 CCATGGCGGCTCCTGCTGTGCTTCTGCTCCTGTGCGGAGTAGTGGATTTCGCCAGAAATTTGAGTATCACTACT
 CCTGAGAGAGATGATTGAAAAAGCCAAAGGGGAAATGCCTATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGTGGATCAAGTGATTATTTTAT
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCGGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGATGCATCAATAAATGTAACGAATTTACAACTGTGCAGATATTGGCCATATCAAGTGCAGAAAGTAA
 AAAAGCTCCTGGTGTTGCAAAATAGAAGATTCACTGGTAGTCTTGTGTTAAGCCCTTCAGGTGCGAGATGTTACG
 TTGATGATCTGAGAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG
 TATGAGTGGCAAAATTTGTCTGACTCACAGAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTA AAAAATGCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGCGCTAAACGTTGTCCCTCCTTCAAATAAAGCTGGACTAATTGCAAGGAGCCATTATAGGAACT
 TTGCTTGCTCTAGCGCTCATTGGCTTTATCATCTTTTGCTGTGCTGTA AAAAGCGCAGAGAAGAAAATATGAAAA
 GGAAGTTCATCAGATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCCTGCCAGAAAGCTACATCG
 GCAGTAATCATTTCATCCCTGGGCTCCATGTCTCCTTCCAACTGGAAGGATATTTCCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCCCTTACAA
 GACTGATGGAATTACAGTTGTATTAATATGGAAGTCTGAAGTATTTGATTATTTGACTTTATTTT
 AGGCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAGGCGACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTATGCAATTGGCATTAGACATGTAAGTCAGATGTCTGTCAAAATTAGTACGAGCCAAATCTTTGT
 TAAAAAACCCCTATGTATAGTGACACTGATAGTAAAAAGATGTTTTATTATATTTTCAATAACTACCATAACAA
 ATTTTTAACTTTTCATATGATATTTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAATTTCTTACGTTCTGTGTTTAAATGTTTTGCTATTTAGTTAAATACATTGAAGGGAATACCCG
 TTCTTTCCCTCTTTATGACACAAACAGAAACACGCGTTGTCATGCTCAAACTATTTTTTATTGCAACTACA
 TGATTTACACAAATTTCTTAAACACAGCATAAATAGATTTCTGTTATATAAATACTTACATACGCTTCCA
 TAAAGTAAATTTCAAAGGTGCTAGAACAAATCGTCCACTTCTACAGTGTTCCTGATTTCCCAACAGAGTTGATGC
 ACAATATATAAATCTCAAGTCCAATATTTAAAAAATCTAGGCACTTGACTAACTTTAATAAAATTTCTCAAACATA
 TATCAATATCTAAAGTGATATATTTTTTAAGAAAGATATTCTCAATAAATCTTCAATAAATAAAGTTTGATGG
 TTTGGCCCTCTAACTTCACTACTATTAGTAGAACTTTTAACTTTAATGTGATAGTAGGTTTATCTCACTT
 TTTCTCAACATGACACCAACCAATCAAAAACGAAGTTAGTGAGTGCTAACTGTGAGGATTAATCTCAAGTAT
 TCCGGTCACAATGCATTCAGGAGGAGGTACCCATGTCACTGGAATTGGCGATATGTTTTTTTCTTCTCCCT
 TGATTTGGATAACCAAAATGGAACAGGAGGAGGATAGTATTCGATGGCCATTCCCTGCATACATTTCTTGCTT
 TTTCTGGGCAAGGGTGCCACATTTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACAT
 TAAGTTAATCAAGGAAAAAATCATCTATGTGCCAGATTCTCATTAAGACAAAGTTACCCACAACT
 GAGATCACTCTAAGTGACATCTCTATTGTCAAGTCTAATAATCTTAAAAACCTCATGTGTAATAGGCGTATA
 TGTATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAATCTCAACACAGTACTTCTTAACAA
 CTTCAACCAAAAAGACCAAACTGGAACGAATGGAAGCTTTGAAGGACATGCTGTTTTTGTAGTCCAGTGGTTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTAAATACAAAACATTTGGAGGTGGAGGCCATTATCCTT
 AGCAACATTAATGCAGAAACAGAAAATCAACTATACGCTATGTTCTCACTTATAGTGGGAGGTAATGATAAAGAACT
 TATGAACACAAAGGAAGGAAACAAATGACATTTGGAGTCTATTTGAGAGGGGAGGGTGGGAGAAAGAAAAGGAGCA
 GAAAGTAACATTTAGTACTGCTTTCACACTCTGGGTGATGAAATATATGTACAAACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAACTCTCATGTGATCCCTAAACCTAAATATAAAGTAAAAA AAAAAAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0990733-1201

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MAILLLCFVLLCGVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLQLSDIGTYQCKVKK
APGVANKKIHLLVVLVKPSGARYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMP
SWLAEMTSSVISVKNASSEYSCTYVNRVSGDQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTCAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCCG
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTACCCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTGTTCCTCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACAGTGCCTGGCTGCTGCAGCAGGAGGTTCTGCAGAACGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTACTCTGGCCAACAACCT
 TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCGAAAATCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTCA
 AACAGTCTCCCTTCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT
 TTGGCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACTTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTTGGGGTGGGGGTAAAGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCAGCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMVMVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

09989733.112001

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACCTTTTCCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGCTTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAAATCCATATTTTACCTATGA

322/330

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSEFLYMQKTLRQCCEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

0000733 11001
100211 11001

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAAACCTTATGTATCATACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
 GGTTCATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTGGATCACACTATTTTCGAC
 CCGGAGAACTGCAGGTTCCAAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACCTCTCC
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACC
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTACAGAGGCTCCCAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTGC
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTFAPASCSEQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCCGTATGACTTAGCACCAGCGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGCCCATTCAGAAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCCCTTTCGACGGCCCCCATCCAGTCATC
 ACCCGTACAGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
 GGTCCCGGATCTGATGTACTCTCTCGCTGAAGCCTGGTGACTGTACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCAGCATCCCTGGGGCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGAAAACACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGCTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTACACC
 CTTAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGAC**CTGA**TGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGGCTA
 ACGGACATCAGTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGTTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
 CGGAGTGATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCCTGCA
 TTAATACTCACTCAGTGTGGCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
 TTVQTTITGSDPEEAIFDTLCTDDSSSEAKLTMDILTTLAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEFPSY
 VKVSGAAPVSIIEAGSAVGKTTSFAGSSASSYSPSEAALKNFPTSETPTMDIATKGPFPSTRD
 PLPSVPPTTTNSSRGNTSLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

09989733-112001

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCCGGTCTTCCGCGCG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGTCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCGTCTAGTCAGAATT
 GCCTCAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCTATTGAAACCGACA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCGAGAAATTTGCCAAG
 CCAAGAGTTACCCCGAGGAAGATTCTCTCTTACATGGCCAATTTTACAAGCAGTCACCTCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCAGTCCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGGTACTCCAAAGCCCGCCACCTTCTACCCCAATGCTTCAGTGACACC
 TTCTGGGCAATTCCAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCATGTCACTTCTC
 AGCCTCCCACGACCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTACAGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCCGAATCACTCCGACAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTCAGTATCCACCTCTCGGCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAAATTAGGTAATTTTGGGTAATCTGCTCTTAAATATAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTTATCAATTTCTAATGAGATTGCTTTCTTTTTATATGAGATTCTTTAAAACTTATT
 CCAGATGTAGTTTCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEI AHLLENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWL LIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGGTGTCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCTGAAGGGGACACTGTGT
 CCTTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGCTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTGCTTGGCACCATCTATGCAGAAGAAGAGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGTCAATTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCAGCCAAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTGGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGCTGCTGAGCCTTCTGTCAAG
 CGCAGGCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGGAGAAAGGAAGCTCAACACCTCAGAG
 CGGAGACACAGAGGAACGAAAGTTCTGGCTTCTCAGCTTGCAGTGGGAGGAAAGGAAGCC
 CCTTCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCATTCCGAAAGTTTCCACCTCAGCCTCAGAGT
 TCCAGTGCCTCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCCTCTTGATGTTTCCA
 GCCTGACCTAGAAGGCTTTGTGACCCCTGGAGCCCAAGCGGTGGCCTTGCTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTATGCCAGTGTGCGACCCTGCCCTTCCCTCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACCTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGACG
 GACTCTGAATTTCTAACAATGCCAGTGAAGTGTGCACTTGAAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTTGGGGTGTGACGCTTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCTTGGTCAGGTCAAGTGCACATTCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCCTTNCATTTGCCCTCCCTGGNCCATGCTTCTTGCCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCCCTTGTCTGGAAGGGTTACTTGCCATATGGGTCTTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTCGAGAAAGGGTTCGGGGGTGGTGGTAAAGTA
 GCACAACCTATATTTTTTTCTTTTTCCATTATATTTGTTTTTAAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCCTGGGTCTCAAGTATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAC
 CTCAAATGAGCCTCCTGCTTCTCAGTCTCCCAAAATGCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTGATGATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAAGAAAAAATGTACCCTATAGTCTCACAGAGACTATCAT
 TATTTTGGTTTTTGTGTACTTCTTCCACTATTTTCTTCTTCACTAATTTTCCGGTGTCTT
 TTTACAGAGCAATTATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAA

